

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 21:18:18 ; Search time 4166 Seconds
(without alignments)
10816.935 Million cell updates/sec

Title: US-09-826-909-1_COPY_232_1161

Perfect score: 930

Sequence: 1 gtgacatgggcaacgaggg.....ggatgcattagaagagggc 930

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_scs.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	930	100.0	1364	AX376727	AX376727 Sequence
2	930	100.0	309400	6 AX127153	Sequence
3	930	100.0	325651	1 AP005283	AP005283 Coryneb
4	930	100.0	349115	1 BX927156	BX927156 Coryneb
5	924	99.4	924	6 BD165429	BD165429 Novel pol
6	924	99.4	924	6 AX123312	AX123312 Sequence
7	439	47.2	439	6 AX376729	AX376729 Sequence
8	399	42.9	302070	1 AP005223	AP005223 Coryneb
9	146	15.7	110000	1 AP006618_15	Continuation (16 o
10	146	15.7	110000	1 AP006618_16	Continuation (17 o
11	132.8	14.3	7846	1 AF116906	AF116906 Rhodococc
12	132.8	14.3	80609	1 AF116907	AF116907 Rhodococc
13	132.8	14.3	80610	1 AP001204	AP001204 Rhodococc
14	130.2	14.0	302325	1 AE017236	AE017236 Mycobacte
15	129.6	13.9	77534	1 AF235504	AF235504 Streptomy
16	129.6	13.9	77536	6 BD235937	BD235937 Polyketid
17	129.6	13.9	77536	6 AR271638	AR271638 Sequence
18	129.6	13.9	77536	6 AR564393	AR564393 Sequence
19	121.2	13.0	292100	1 SC0939121	SC0939121 Streptomy

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	22	95.6	10.3	180136	1	BAC180K	D26185 B. subtilis
	23	95.6	10.3	203901	1	BSUB0021	Z99124 Bacillus su
	24	86.6	9.3	110000	1	AP006840_22	Continuation (23 o
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	26	80	8.6	300854	1	AE017014	AE017014 Bacillus
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	40	68	7.3	11015	1	AE004736	AE004736 Pseudomon
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C	44	65.2	7.0	349008	1	BX640444	BX640444 Bordetell
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ALIGNMENTS

RESULT 1	AX376727	AX376727	1364 bp	DNA	linear	PAT 18-MAR-2002
LOCUS	Sequence 1 from Patent WO0212504.					
DEFINITION	AX376727					
ACCESSION	AX376727.1	GI:19573112				
VERSION						
KEYWORDS	Corynebacterium glutamicum					
SOURCE	Corynebacterium glutamicum					
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.					
REFERENCE	1					
AUTHORS	Moockel, B., Farwick, M., Hermann, T., Kreutzer, C. and Pfefferle, W.					
TITLE	Nucleotide sequences which code for the lysr2 gene					
JOURNAL	Patent: WO 0212504-A 1 14-FEB-2002;					
DEGUSA AG (DE)						
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ORIGIN

Query Match	100.0%	Score	930;	DB	6;	Length	1364;
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Matches	930;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
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Qy 241 GTGCGAGAAATCAACTCGCGCGCACTGAATCAAACTCAAACTCAAACTCAAACTCAAA 300
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RESULT 2
AX127153/c 309400 bp DNA linear PAT 11-MAY-2001
LOCUS
DEFINITION
Sequence 7069 from Patent EP1108790.
ACCESSION AX127153 AX114121
VERSION AX127153.1 GI:114041141
KEYWORDS
Corynebacterium glutamicum
SOURCE
Corynebacterium glutamicum
ORGANISM
```

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.

REFERENCE
1
AUTHORS Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K.,
Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.
TITLE Novel polynucleotides
JOURNAL Patent: EP 1108790-A 7069 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)

FEATURES
Location/Qualifiers
source
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ORIGIN

Query Match 100.0%; Score 930; DB 6; Length 309400;
Best Local Similarity 100.0%; Pred. No. 8.9e-212;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match 100.0%; Score 930; DB 1; Length 325651;
Best Local Similarity 100.0%; Pred. No. 8.9e-212;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

LOCUS BX927156/c

DEFINITION Corynebacterium glutamicum ATCC 13032, IS fingerprint type 4-5,

complete genome; segment 9/10.

ACCESSION BX927156 BX927147

VERSION BX927156.1 GI:41326831

349115 bp DNA linear BCT 10-JUN-2004

KEYWORDS
SOURCE
ORGANISM

complete genome.
Corynebacterium glutamicum ATCC 13032
Corynebacterium glutamicum ATCC 13032
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
1 (bases 1 to 349115)

REFERENCE
AUTHORS

Kalinowski, J., Bache, B., Bartels, D., Bischoff, N., Bott, M.,
Burkovski, A., Dusch, N., Eggeling, L., Eikmann, B. J., Gaigalat, L.,
Goesmann, A., Hartmann, M., Huthmacher, K., Kramer, R., Linke, B.,
McHardy, A. C., Meyer, F., Mockel, B., Pfeifferle, W., Puhler, A.,
Rey, D. A., Ruckert, C., Rupp, O., Sahm, H., Wendisch, V. F., Wiegand, I.
and Tauch, A.

TITLE

The complete Corynebacterium glutamicum ATCC 13032 genome sequence
and its impact on the production of L-aspartate-derived amino acids
and vitamins

J. Biotechnol. 104 (1-3), 5-25 (2003)

JOURNAL
MEDLINE

22830012

PUBMED

12948626

2 (bases 1 to 349115)

REFERENCE
AUTHORS

Kalinowski, J.

TITLE

Direct Submission

JOURNAL

Submitted (21-JAN-2004) Joern Kalinowski, Institut fuer
Genomforschung, Universitaet Bielefeld, Universitaetsstrasse 25,
33615 Bielefeld, Germany
E-mail: Joern.Kalinowski@cebitec.uni-bielefeld.de
This sequence was accomplished by collaboration between Degussa AG
and Bielefeld University.

COMMENT

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gene

CDS

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QY 121 CTTTCCAGAGCAATCAGCGAGTGGAAACACGAGGACCCCACTTTTCGACCGCGC 180
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DB 307784 ACATTCCGCGCGCAACACCCCAACGTAAGATTCCAATCTCCACCAAGCGGAGCAATGCTC 307725

QY 421 CTGCTAGATCGTGTGTTTGGCTGATGAACCTCGACTAGTCTAGTGGCCCCAAACCTGCC 480
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QY 841 TTGGTGTGGGACTCAACCGGGGCGGCACCTCGCGTGGATAACTCCGGAAGTTCGTG 900
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LOCUS
DEFINITION Novel polynucleotide.
ACCESSION BD165429
VERSION BD165429.1 GI:27871241
KEYWORDS JP 2002191370-A/3228.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 924)
AUTHORS Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
Yokoi,H., Tateishi,N., Senoo,A., Ikeda,M. and Ozaki,A.
TITLE Novel polynucleotide
JOURNAL Patent: JP 2002191370-A 3228 09-JUL-2002;
KYOWA HAKKO KOGYO CO LTD
COMMENT OS Corynebacterium glutamicum
PN JP 2002191370-A/3228
PD 09-JUL-2002
PF 15-DEC-2000 JP 2000405096
PI SATOSHI NAKAGAWA,HIROSHI MIZOGUCHI,SEIKO ANDO,MIKIO HAYASHI,
PI KEIKO OCHIAI,
PI HARUHIKO YOKOI,NAOKO TATEISHI,AKIHIRO SENOO,MASATO IKEDA,AKIO
PI OZAKI
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LOCUS Sequence 3228 from Patent EP1108790.
DEFINITION AX123312
ACCESSION AX123312
VERSION AX123312.1 GI:14040800
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REFERENCE
    1 Nakagawa S., Mizoguchi H., Ando S., Hayashi M., Ochiai K.,
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LOCUS AX376729 439 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 3 from Patent WO212504.
ACCESSION AX376729
VERSION AX376729.1 GI:19573114
KEYWORDS Corynebacterium glutamicum
SOURCE Corynebacterium glutamicum
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.

REFERENCE
AUTHORS Moeckel, B., Farwick, M., Hermann, T., Kreutzer, C. and Pfeifferle, W.
TITLE Nucleotide sequences which code for the lysr2 gene
JOURNAL Patent: WO 0212504-A 3 14-FEB-2002;
Degussa AG (DE)
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DB 361 CTGGCGGGAAGAACCTTTCTGTCGATGCGAGCAGGTTTCGGCACCCGACTTCTCATGG 420
QY 656 ATGCATTAGCGGAAGAGC 674
DB 421 ATGCATTAGCGGAAGAGC 439

RESULT 8
AP005223/c
LOCUS AP005223 302070 bp DNA linear BCT 24-JUL-2003
DEFINITION Corynebacterium efficiens YS-314 DNA, complete genome, section 10/11.
ACCESSION AP005223 BA000035
VERSION AP005223.1 GI:23494433
KEYWORDS Corynebacterium efficiens YS-314
SOURCE Corynebacterium efficiens YS-314
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.

REFERENCE
AUTHORS Nishio, Y., Nakamura, Y., Kawarabayasi, Y., Usuda, Y., Kimura, E., Sugimoto, S., Matsui, K., Yamagishi, A., Kikuchi, H., Ikeo, K. and Gojobori, T.
TITLE Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium efficiens
JOURNAL Genome Res. 13 (7), 1572-1579 (2003)
MEDLINE 22723752
PUBMED 12840036
REFERENCE 2 (bases 1 to 302070)
AUTHORS Kawarabayasi, Y., Yamazaki, J., Hino, Y., Kikuchi, H. and Director-General of Biotechnology Center.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2002) Director-General of Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; Nishihara 2-49-10, Shibuya-ku, Tokyo 151-0066, Japan (E-mail: bio@nitech.go.jp, Tel: 81-3-3481-1933, Fax: 81-3-3481-8424) Kawarabayasi, Y. is officially affiliated with the National Institute of Advanced Industrial Science and Technology, Tsukuba, Ibaraki, 305-8566 Japan
Nakamura, Y., Ikeo, K., Suzuki, M. and Mashima, J. are at the National Institute of Genetics, Mishima, Shizuoka, 411-8540 Japan
Itoh, T. is at the Japan Biological Information Research Center, Koko-ku, Tokyo, 135-0064 Japan
Yamagishi, A. is at Tokyo University of Pharmacy and Life Science, Hachioji, Tokyo, 192-0392 Japan
Nishio, Y., Usuda, Y. and Sugimoto, S. are at the Ajinomoto Co., Inc., Kawasaki, Kanagawa, 210-8681 Japan
The other authors are at the National Institute of Technology and Evaluation, Shibuya-ku, Tokyo, 151-0066 Japan.
LOCATION/Qualifiers
1. .302070
/organism="Corynebacterium efficiens YS-314"
/mol_type="genomic DNA"
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/db_xref="taxon:196164"
complement(52..1248)
/note="CE2590, similar to X89084-2|CAA61456.1| percent

FEATURES
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1. .302070
/organism="Corynebacterium efficiens YS-314"
/mol_type="genomic DNA"
/strain="YS-314"
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CDS

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ALYANKOVAEYGRIRYFGHGTSHYSSRVVDLMDKPABEINTITHLNGASMAA
VKGAVNDTSMGTPLAGVMCTRTGDIDPGVVFLARNANMSIDEIDNLMNKKSGVK
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DKLKAARNHGLEPVMGAALFENMLKRAKEQAHIVLPEGEDDRILMAAHLLEKD
ICELTILGDEOIHSGRATBLGLHLEKADVINTLPDKLDEPAEQFAELRKSGITLEQ
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DLMKSDHDVQDLFERMAPFGLTRYGAPDHPRIKGLVKSLLHNVLQEKURLGNI
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SWLSAEKAVFVGVGNALDVARIILAKTGDLEKVTETPDNVYESLONKAREVHFGR
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VYRAGVSDAIVRDPDDERAILINDGGRVIDPSTGSPVTSLYATGHIKRGPIGLIG
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complement (5283..6560)
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identity: 86 in 401 aa"
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FCSTFEETFAAERLGPVNVKPVMSGSGQSVTSADLESAMEYASGRVSNQR
VIVEQFVEPDYEITLLTVRGIDPATGKPATWCFEPIGHRQDQDGVESWQPMEMTAPA

CDS
LENASVAARITNALGGRGVFGVELFVSEVSPRPHDTGLVTLATQRFSEFE
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6584..7768
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identity: 38 in 391 aa"
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LQGHVMAQGVISMPETAKVMTESIRVRVFGTGHGSMPLHGVDPVILAHHIITRL
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VSCEEAAGCAEPTFEYDRAPLTFNDADARSVVAEAFNQAFGEYQVTPSTASED
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7827..8417
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identity: 61 in 429 aa"
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BSALDVKQVLAVKYNRAIYAEETVOYELSYADRLRPMVIDATLELAKALDEGKHLV
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TGGEIPICVAYEVDVGRHDEMPMTQSDPFHAKPIFETMPAMDEDTGCRTFEELPQK
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10063..10989
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identity: 20 in 247 aa"
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PEQRIIRIVIGDSLSAVITRLMRADNMMAEVAVYPTGESVAAKMGLPADPGALR
LALTCAKVPVPTIRDDAAVAVAGSATITDWEPEITGEIIVDDHVLVRHEASPKTPRR
GIFGARLYPMVAVGIAAAMVMDTPAGTEIKKGLFRRPTGTTLIPESLSTGRATQAGGP
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CDS complement(11200..12426)
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identity: 74 in 359 aa"
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Query Match 42.9%; Score 399; DB 1; Length 302070;
Best Local Similarity 66.4%; Pred. No. 1e-84;
Matches 592; Conservative 0; Mismatches 290; Indels 9; Gaps 1;

QY 27 CTGCGAATCGACGACCTACGAGCTTCATTTTCAGTCGCTCAATCAGGCCACCTCACCGA 86
Db 194739 CATGAGATCGATGATCTCCGCTTTTCATCGAGTTCGCGAGTCCGGCACCTGACGGA 194680

QY 87 AACTGCCGAAAGATTAGGATCCCGAGCCGACACTTTCCAGACCAATCAGCCGAGTGA 146
Db 194679 GACGCGGATCGGCTCGGTATTTGCGCAGCCGACACTGTGCGCCGAGATGGCGCGTGA 194620

QY 147 AAAACACGAGGACACCCCACTTTTCGACGCGCGCGCGCAAACTCGTCTCAACCAACG 206
Db 194619 AAGACAGTGGTAGCGCGCTGTTGAGCGCGCGCGCGAGCTCCAGCTCAACCCCGG 194560

QY 207 AGGCACGCTTCTTCAACACGCGAGCGCCATCGTCGAGAAATCAACTCGCGCGCAAC 266
Db 194559 CGGGCAGGCTTCTTCCACACGCGCGCGCATCACCGGAGCTGGAGTGGCGGTCAAC 194500

QY 267 TGAATCAACGCTCATGGACCCAGAAAAGGCAATCCGACTGGACTTCATGCTATTC 326
Db 194499 GCAGTCAACGCTCGATGGACCCGAGCTGGGACAGTCCGCCCTGGGATTTCAATGCTTC 194440

QY 327 CTTGGGCACTTGGATGGTCCCGAACTTATCCGAACTTCCGCGCGCAACCCCAAGT 386
Db 194439 GCTGGGCACTGGATGGTCCCGAGCTGATCCGTAATCCGACCGACCCCGCGGT 194380

QY 387 AGAATTCACACTCCACCAAGCGGACCAATGCTCTCGTGTAGATCGTGTGGCTGATGA 446
Db 194379 GGAGTTGAGTGCACACGAGGCGCGCAATGAGTGGTGGCGCGTGTGACGACGC 194320

QY 447 AACTGACCTCGATTAGTTGGGCCCCCAACCTCCGAGGTGTGACTCTTTAGGGTGGC 506
Db 194319 CGCCGACCTCGCCCTCGTGGGACCGAGACCCGCGAGGTGCGACGTGTGTGGGTGGC 194260

QY 507 GCACTGCTTCTCAACGACTTGCCTAGCTTCCCGCAGATCACCGGCTTGCCTCCTT 566
Db 194259 GCGCTGCTGCGCAGGCTCTGCGCTGCGCGGCGCACCGCTCGAC----- 194205

QY 567 TTCTGCGCAAGAGAAATTCGCTTGAATTCGCGCGGGAAGAACTTTCTGTGGCGATGCG 626
Db 194204 ----GGTGGAGCGCGTGCAGCTGGGAGGCTGCGGGGAACTTCTGTGGCGATGCT 194149

QY 627 AGCAGGTTTCGACCCGACTCCTCATGATGCATTAGCCGAAGCGGGTTTGTTC 686
Db 194148 GCGCGTTTCGCAACCGCGCTGCTTCTGACGCCCTGGCCACCGCTCGGTATCACCCC 194089

QY 687 CAATGTGTTTTGCAATCATGAACTCACACCGCTCGCAGGCTTGTGAGCGCAGGTCT 746
Db 194088 CGACATCGTTCGAATCATGAACTGACACCGCTCTCGGCTGTGTGAGCGCAGGTCT 194029

QY 747 CGCGCTGTGTGGTTCGATGGATGATCCGTAATCTCCACAGTGGGAATCGTGAACG 806
Db 194028 GGGCGTGGCGTGTGCTGCCATGGGCGATCCACACCTGCCACCGTGGGCGTGAACCTGG 193969

QY 807 CCCACTTAGTCCACCGCTTATAGGAAGTATGTTTGTGTGGCGCACTCAACGCGGGCC 866
Db 193968 GCGCTTCGAACTGCGACCCCGGAACTCGGCTGTGTGTGGCGGCTGATTCGCGGCC 193909

QY 867 GGCACCTCGGTGGATTAATCTCCGGAAGTTCGTGGCGGATCGAGGTATGC 917
Db 193908 CGCCCGCGGCTGGAGGTGTTCCGGGATTTCTGTGGCGGCTCCCGGTTGC 193858

RESULT 9
AP006618_15

WPCOMMENT
Sequence split into 61 fragments LOCUS AP006618 Accession AP006618

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AP006618_03	300001	410000
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AP006618_05	500001	610000
AP006618_06	600001	710000
AP006618_07	700001	810000
AP006618_08	800001	910000
AP006618_09	900001	1010000
AP006618_10	1000001	1110000
AP006618_11	1100001	1210000
AP006618_12	1200001	1310000
AP006618_13	1300001	1410000
AP006618_14	1400001	1510000
AP006618_15	1500001	1610000
AP006618_16	1600001	1710000
AP006618_17	1700001	1810000
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AP006618_57	5700001	5810000
AP006618_58	5800001	5910000
AP006618_59	5900001	6010000
AP006618_60	6000001	6021225

Continuation (16 of 61) of AP006618 from base 1500001 (AP006618 Nocardia farcinica IFM 1

Query Match 15.7%; Score 146; DB 1; Length 110000;
Best Local Similarity 51.1%; Pred. No. 3.6e-24;
Matches 403; Conservative 0; Mismatches 370; Indels 15; Gaps 2;

QY 15 CGACGGCGGAGACCTCGGATCGAGACCTAGCAGCTTCAATTCAGTCGCTCAATCAGG 74

Db 107923 CGGAGGTGTGGCTGTCTCGCGGAGGACCTGAGGTGGTACACGACACTCGTCGAGACACA 107982

QY	75	CCACCTCACGAAATGCGGAAAGATTAGGCAATCCCGAGCCCACTTTCCAGACGAAT	134
Db	107983	GAGCGTGAGCGCGCGCGCGGTGCACTCGCGAGCGGACCTCTCGCGCATGCT	108042
QY	135	CAGCCGAGTGGAAAAACACGACGACCCCACTTTTCGACCGCGCGCGGCAAACTCGT	194
Db	108043	GGCCCGGCTCGAGCGGAGACTCGGGTGCCTTTTCGACCGCGGCAAAACGATCGC	108102
QY	195	CCTCAACCAAGGAGCGACGCTTCTCAACACGCGGCGGATCGTCGAGAAATCAA	254
Db	108103	GCTCAACGAGTTCGCGCGGCTGCTACGACGCGCGCGGCGGACAGTCCGAGCTCGA	108162
QY	255	CTCCGCGCACTGAATCAAAACGCTCATGGAACCCAGAAAAAGGACCAATCCGACTGA	314
Db	108163	CGCGCGGACAGCGGCTGCGGACCTGGCCGATCCGCGAGGGGCTGCGGCTGTC	108222
QY	315	CTTCATGCAATCTTGGGCACTTGGATGTTCCCGAACTTATCCGAAATTTCCGCCGA	374
Db	108223	GTTCCTGCATTCCTTCGCGGCTGGCTGGTGCCACAGCTGGTCGCGGCTTCGCGCGG	108282
QY	375	ACACCCCAAGTAGAATTCACCTCCACCAAGCGGAGCAATGCTCTGCTAGATCGTGT	434
Db	108283	CGCGCGCGGCTGAGCTGACACTGTGGCAGGCGCGCGGCCACCATCACCGCGCGGT	108342
QY	435	TTTGCTGATGAATGACCTCGCATTAGTTGGCCCAAACTGCGGAGGTTGGTACCTC	494
Db	108343	GCTCGACGGAGCGCGACCTCGGCATGCTCTCGCGCGCGCGGCGTACGGGCATC--	108400
QY	495	TTTAGGGTGGCGCACTGCTGCTCAACGACTGTCCTGAGTTCCTGCGGAGTCAACCG	554
Db	108401	----GGCTGGACCACTGCTGCGCAGCGCGCTCATGCTCGCGGTCCGCGCGGAGCACCG	108456
QY	555	GCTTGCTCTCTTCTGCGCAAGAGAAATTGCGGTTGATTACTGCGCGCGGAGAACTTT	614
Db	108457	GCTGGCC-----GGGCGCGCGAGTGCGGCTGGCGGAGCTGGGCGAGCCGAGTT	108507
QY	615	CGTGGCGATCGGAGCAGGTTTGGCACCGGACTCTCTCATGGATGATAGCCGGAAGAC	674
Db	108508	CGTCAGATGACCCGGGCTTGGGATGCGCGGCTCTTCGATGATCTGTGCGCGCGC	108567
QY	675	CGGTTTGTTCGAATGTGTTTTCGAATCCATGGAATCACCAGCTGCGAGGGTGTGT	734
Db	108568	GGGCATCCCGCGGCTATCGGTTTCGAGTCCAGTCACTGATCACCCTGCGCGGCTGT	108627
QY	735	CAGCGCAGTCTCGGCGTTGCTGCTCCGATGATGATCCGTACTCTCCACAGTGG	794
Db	108628	CGCGCGGCTCGGGTGCCTTGTCTGCGCTGCTGGACCAAGCGCGCCACCACTGCTCG	108687
QY	795	AATCGTCG 802	
Db	108688	GCCGCTGC 108695	

RESULT 10

AP006618.16

WPCOMMENT

Sequence split into 61 fragments LOCUS AP006618 Accession AP006618

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AP006618_02	200001	310000
AP006618_03	300001	410000
AP006618_04	400001	510000
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AP006618_09	900001	1010000
AP006618_10	1000001	1110000
AP006618_11	1100001	1210000
AP006618_12	1200001	1310000
AP006618_13	1300001	1410000

AP006618_14	1400001	1510000
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AP006618_56	5600001	5710000
AP006618_57	5700001	5810000
AP006618_58	5800001	5910000
AP006618_59	5900001	6010000
AP006618_60	6000001	6021225

Continuation (17 of 61) of AP006618 from base 1600001 (AP006618 Nocardia farcinica IFM 1

Query Match 15.7%; Score 146; DB 1; Length 110000;

Best Local Similarity 51.1%; Pred. No. 3.6e-24;

Matches 403; Conservative 0; Mismatches 370; Indels 15; Gaps 2;

QY	15	CGACGCGGAGACCTTGGCAATCGACGACTAGCAGCTTCAATTCAGTTCATTTTCAGTTCATTCAGG 74
Db	7923	CGAGGTGGTGGCTGCTCGCGAGGACCTGAGGTGTGTACAGACACTGTCGAGACACA 7982
QY	75	CCACCTCACGAACTCGGAAAGATTAGGATCCGAGCCCACTTTCCAGACGAAT 134
Db	7983	GAGCGTGAAGCGCGCGCGGCTGCACCTCGCGAGCGGACCTCTCGCGCATGCT 8042
QY	135	CAGCCGAGTGGAAAAACACGAGGCAACCCCACTTTTCGACCGCGCGCGGCAAACTCGT 194
Db	8043	GGCCCGGCTCGAGCGCAGACTCGGGTGCCTTTTCGACCGCGCGGCAAACTCGT 8102
QY	195	CCTCAACCAACGAGCGCAGGCTTCTCTCAACGAGCGGCGGCTGTCGCGAGAAATCAA 254
Db	8103	GCTCAACGAGTTCGCGCGGCTGTACTAGAAACACGCGCGCGGCGGAGCTCGA 8162
QY	255	CTCCGCGGCACTGAAATCAACGCTCATGACCCAGCAAAAGGACACATCCGACTGA 314
Db	8163	CGCCCGCGGACAGCGGCTGGCGGACCTGGCCGATCCCGCGGCGGCTGGTGGCTGTC 8222

QY 315 CTTTCATGCAATCTCTGGGCACTTGGATGTCCTCCGAACTTATCCGAAACATTCGCGCGGA 374
 DB 8223 GTTCTGCAATCTCTGGGCGGCTGGCTGTGTGCACAGCTGTGTCGGGGCTTCCGCGCGG 8282
 QY 375 ACACCCCAACGTAGAAATCCAACTCCACCAAGCGGAGCAATGCTCTCTGGTAGATCGTGT 434
 DB 8283 CGCGCGCGGGTGAGCGTCACTGTGGCAGGCGCGCGCCACCATCAACCGCGCGGT 8342
 QY 435 TTTGGCTGATGAATGACCTGCACTAGTTAGTGGCCCAAACTGCGAGGTTGGTACCTC 494
 DB 8343 GCTCGACGGGAGCGCGCACTCGGCATGCTCTCGCGCGCGCGGCTGACGCGGCATC-- 8400
 QY 495 TTTAGGTTGGGCGCACTCTCTGTCACAGACTTGCCTAGCTGTTCGCGAGATCACCG 554
 DB 8401 ----GGCTGGAGCACTCTCTCGCGAGCGCTCATGTCTCGCGTTCGCGCGCGAGCACCG 8456
 QY 555 GCTTGCTCTCTTTCTGCGCAAGGAGAAATGCGTTGATTAATCTGCGCGGAGAAACCTTT 614
 DB 8457 GCTGGCC-----GGGCGCGCGCAGGTGCGCTGGCGGAGCTGGGCGACGCCAGTT 8507
 QY 615 CTTGGGATGACGAGCAGTTTGGGACCGCACTCTCTCATGATGATTTAGCCGAAGAAGC 674
 DB 8508 CGTACGATGACCGCGGCTTCGGATGCGCGCGCTCTTCGATGATCTGTGCGCGCGCGC 8567
 QY 675 CGGTTTGTTCCTCAATGTGTTTTCGAATCCATGAACTCACACCGCTGCGAGGCTTGT 734
 DB 8568 GGGCATCCGCGCGTATCGGTTTCGAGTCCAGTCACTGATCACTGATCGCGCGCTGT 8627
 QY 735 CAGCGAGCTCTCGCGTTGTGTGTTCGATGATGATGATGATGATGATGATGATGATGATG 794
 DB 8628 CGCGCGCGGCTCGGGTGCCTTGTGCGCGTGTGGACAGGCGGCCACCGTGC 8687
 QY 795 AATCGTC 802
 DB 8688 GCCGTGC 8695

RESULT 11
 AF116906/c
 LOCUS AF116906 7646 bp DNA linear BCT 26-APR-1999
 DEFINITION Rhodococcus equi virulence associated plasmid fragment d sequence.
 ACCESSION AF116906
 VERSION AF116906.1 GI:4680485
 KEYWORDS
 SOURCE Rhodococcus equi (Corynebacterium equi)
 ORGANISM Rhodococcus equi
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Nocardiaaceae; Rhodococcus.
 Hines,S., Alperin,D., Prescott,J. and Nicholson,V.
 1 (bases 1 to 7646)
 Sequence of fragment d of 85 kb virulence associated plasmid of
 Rhodococcus equi strain 103
 Unpublished
 JOURNAL
 REFERENCE 2 (bases 1 to 7646)
 Hines,S., Alperin,D., Prescott,J. and Nicholson,V.
 Direct Submission
 TITLE Submitted (29-DEC-1998) Veterinary Microbiology and Pathology,
 JOURNAL Washington State University, PO Box 647040, Pullman, WA 99164-7040,
 USA
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ORIGIN

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 Best Local Similarity 51.1%; Pred. No. 5.4e-21;
 Matches 373; Conservative 0; Mismatches 342; Indels 15; Gaps 2;

QY 35 TCGACGACCTAGCGAGCTTCAATTCAGTCGCTCAATCAGGCGCACCTCACGAAACTGCGG 94
 DB 3952 TTGACGAATCTCGCTGGTTTGGGTTTAGCAGAAATCGAGCACATGCGCGATGCGGGTGG 3893
 QY 95 AAAGATTAGGCATCCCGCAGCCACACTTTTCCAGACGAATCAGCGAGTGGAAACACG 154
 DB 3892 ACGCCCTGCACATCTCTCAACCGACTCTCTCGCGGGCGCTTGCCTGCGCATTTGAACGACAGG 3833
 QY 155 CAGGACCCCACTTTTGGACCGCGCGCGCGCAAACTGCTCTCAACCAACGAGGCGCAGG 214
 DB 3832 TTGGGGTGGCGCTGTTCGATCGGGTGAACCATCGCTGACGCTCAACGACTACGCGCGGA 3773
 QY 215 CTTCTCCCAACCGCGCGCGCGCGCAAACTTCAACTCGCGCGCAACTGAAATCA 274
 DB 3772 TCATGCTTGACATCTCGCGGAGTTTGACCGAACTCCACTCAGCGCGCGGAGGATCG 3713
 QY 275 AACGCTCATGAGCCCGAGAAAGGCAAAATCCGACTGGAATTCATGCAITTCCTTTGGGCA 334
 DB 3712 CTGCGCTCGTAATCTCTGAGTCAGGACCGCTTCGCTAGGCTTCTGCACTCCCTTGGCA 3653
 QY 335 CTTGATGGTCCCGAACTTATCGAATTCGCGCGCGCAACACCCCAACGATGAAATCC 394
 DB 3652 GTTGGTTTGTGCTGAGATCATCGGGGTGTTTCGCGAGAGCGCGCGAGGCTGAACCTTCG 3593
 QY 395 AACTCCCAAGCGCGAGCAATGCTCTGCTGATGATCGTGTGCTGATGAACTGACC 454
 DB 3592 CGCTGAAACGAGCTCCGAGCGAGGCAATCGAAGCGATGCTGCTCGGGGAGATTTGATG 3533
 QY 455 TCGCATTAGTTGGCCCCCAACCTCCGAGGTTGATGCTCTTTAGGGTGGCGCACTGC 514
 DB 3532 TCGCAGTGTATCGGCGCACCGCGCGCGG-----ACGAGTTGAGTGTATGAGCTCT 3479
 QY 515 TTCGTCAACGACTTGGCTTCCGCGAGATCACCGGCTTGCCTCTCTTTCTGGCC 574
 DB 3478 ACGTAGAACGCTTTCCTGCTGCGGGAATCTCACC-----CCTTAGCGGGC 3428
 QY 575 AAGGAGAAATGCCGTTGATTACTCGCGCGGAGAAACCTTTTCGTCGCGATGCGAGCAGTT 634
 DB 3427 GTGCGACTATCGGATAGCAGACGCTTCGATACGCTTTCATATGCTCCGAGGCCAT 3368
 QY 635 TCGGACCCGACTCCTCATGGATGATGATGATGATGATGATGATGATGATGATGATG 694
 DB 3367 TCGGCTCGCAAGCTGTGTCGCAAGCTGTTTCGCGGCTGCTGGCTCGTACCCCAATCG 3308
 QY 695 TTTTCGATCCATGGAATCACACCGCTCGCAGGCTGTGTCAGCGAGTCTCGGCGTTG 754
 DB 3307 TCTTTGAGACATCGAGATCCCTACCTCGAGGCGCTGTTGGCGGCTTCGGGGTTCG 3248
 QY 755 GTGTGGTTCC 764
 DB 3247 CTGTGGTTCC 3238

RESULT 12
 AF116907
 LOCUS AF116907 80609 bp DNA circular BCT 07-FEB-2001
 DEFINITION Rhodococcus equi virulence plasmid, complete sequence.
 ACCESSION AF116907 AF077324 AF077325 AF116908 AF118815 U60204
 VERSION AF116907.2 GI:10657865
 KEYWORDS
 SOURCE Rhodococcus equi (Corynebacterium equi)
 ORGANISM Rhodococcus equi
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Nocardiaaceae; Rhodococcus.
 1 (bases 6847 to 6906)
 de la Pena-Moctezuma,A. and Prescott,J.F.
 A physical map of the 85 kb virulence plasmid of Rhodococcus equi
 103
 JOURNAL Can. J. Vet. Res. 59 (3), 229-231 (1995)
 MEDLINE 96131066
 PUBMED 8521357
 REFERENCE 2 (bases 6847 to 6906)
 Zhenh,H., Tkachuk-Saad,O. and Prescott,J.F.


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Query Match 14.3%; Score 132.8; DB 1; Length 80609;
Best Local Similarity 51.1%; Pred. No. 5.2e-21;
Matches 373; Conservative 0; Mismatches 342; Indels 15; Gaps 2;

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QY 35 TCAGCACTACGACGCTTCATTTCAGTCGCTCAATCAGCGCACCTCACCGAACTGCGG 94
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
4949 TTGACGAACCTCGCTGTTGTGTGGCTTAGCAGATCGGAGCACATGCGCGATGCGGCTG 5008
QY 95 AAAGATTAGGATCCGCGAGCCACATTCAGTCAGAGATCAGCGAGTGGNAACACAG 154
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
5009 ACGCCTTGACATCTCTCAACGACTCTCTCGCGGGCGCTTGCCCGCATTTGAACACAGG 5068
QY 155 CAGGCACCCCACTTTTCGACCGCGCGGCGCAAACTCGTCTCAACCAACGAGGCCACG 214
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
5069 TTGGGGTGCCCTGTGTGATCATCCGGGTGACCATCGCTGCGCTACGACTAGCGCCGGA 5128
QY 215 CTTCTCTCAACCAACGCGAGCCATCGTCGCGAGATTCACATCCCGCGCAACTGAATCA 274
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
5129 TCATGCTTGAGCATACTCGCGGAGTTTGACCGAACTCCACTCAGCGCGGAGCGGATCG 5188
QY 275 AACGCTCATGACCAAGAAAGGACATCCGACTCGACTTCATGATCTCTTGGGCA 334
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
5189 CTGCGCTCGTAATCTGAGTCAGGACCGTTTCGCGTAGGCTTCGTCACCTCCCTTGGCA 5248
QY 335 CTTGGATGTCCTCCGAATTCATCCGAACATTCGCGCGCGCAACACCCCAACGTAGAATCC 394
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
5249 GTTGGTTGTGCTGATCATCCGGGTGTTTCGCGAGAGCGCGCGAGGTGAATTCG 5308
QY 395 AACTCCACCAACGCGGAGCAATGCTCTGTTGATAGTCGTGTTTGGCTGATGAATGACC 454
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
5309 CGCTGAACACGAGCTCCGACGAGGCGCATCGAAGCGATGCTGCTCGGGGAGATTGATG 5368
QY 455 TCGCATTAGTTGGCCCAACCTCGCGAGTTGGTACCTCTTTAGGTTGGGCGCCATGCG 514
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
5369 TCGCAGTGTATCGGCGCACCGGCCCGCGCGG-----ACGAGTTCAGCTGATGAGCTCT 5422
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QY 515 TTGCTCAACGACTTGCCCTAGCTGTTCCGCGAGATCACCGGCTTGCCTCTTTCTGGCC 574
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5423 ACGTAGAAGCTTTGCTTCGCTGCTGCGCGAATCTCACC-----CCTTAGCGGCG 5473
QY 575 AAGGAGAATTGCCGTGTGATTACTGCGGCGGGAAGAACCTTTCTGTGCGGATGCGAGCAGTT 634
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
5474 GTGCGACTATCGGATAGCAGACGCTTCGATAAGCGCTTCATTATGCTCGCAGGCCAT 5533
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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5594 TCTTTGACGATCGAGATCCCTACCTCGAGGCGCTGTGCGCCGACGTTTCGGGGTCG 5653
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
5654 CTGTGTTTCC 5663

RESULT 13
AP001204 80610 bp DNA circular BCT 29-NOV-2000
LOCUS Rhodococcus equi plasmid pREAT701 DNA, complete genome.
DEFINITION AP001204
ACCESSION AP001204
VERSION AP001204.1 GI:10801055
KEYWORDS Rhodococcus equi
SOURCE Rhodococcus equi
ORGANISM Rhodococcus equi
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Nocardiaceae; Rhodococcus.
REFERENCE 1 (sites)
AUTHORS Takai,S., Hines,S.A., Sekizaki,T., Nicholson,V.M., Alperin,D.A.,
Osaki,M., Takamatsu,D., Nakamura,M., Suzuki,K., Ogino,N.,
Kakuda,T., Dan,H. and Prescott,J.F.
TITLE DNA sequence and comparison of virulence plasmids from Rhodococcus
equi ATCC 33701 and 103
JOURNAL Infect. Immun. 68 (12), 6840-6847 (2000)
MEDLINE 20536428
PUBMED 11083803
REFERENCE 2 (bases 1 to 80610)
AUTHORS Takai,S., Sekizaki,T., Kakuda,T., Nakamura,M., Suzuki,K. and
Ogino,N.
TITLE Direct Submission
JOURNAL Submitted (18-FEB-2000) Shinji Takai, Kitasato University, School
of Veterinary Medicine and Animal Sciences, Department of Animal
Hygiene; Higashi 23-35-1, Towada, Aomori 034-8628, Japan
(E-mail:takai@vmas.kitasato-u.ac.jp, Tel:81-176-23-4371(ex.459),
Fax:81-176-23-8703)
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overlap) ; DAD:z95557-4"
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15-17kDa antigen(189 aa) 4.7e-23(47.541% identity in 183
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TYDFAEAGSGSIPAKVAEQAQNSYSHGLVTSLAYVQHFSLTVEGGGTFTGDSGGI
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overlap) ; DAD:u82598-30"
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QY 436 TTGGCTGTAGTAAACTGACCTCGCATTTAGTTGGCCCCCAACCTGCCGAGGTTGGTACCTCT 495
Db 12262 CGGTCCGGCGGTGACATCGGCTGGTATCCCCCGACCGTTCGAG-----CGAAC 12315
QY 496 TTAGGGTGGGCGCACTGTTGTCACACACTTGCCTAGCTGTTCCCGCAGATCACGG 555
Db 12316 CTGGCTGGCGCAGCGCTGTTTCGCCAGCGCCTCGGTGTCGGGTGCCGATGTCATCGA 12375
QY 556 CTTGCTCTCTTTCTGGCCAAAGAGAAATTGCCGTTGATTACTGCCGCGGAGAAACCTTTC 615
Db 12376 TTCGCC-----CGCGGTCCGGGTGTCATGTTGGACCTGCCGACGAGCCCTTC 12426
QY 616 GTGGCGATCGAGCAGGTTTCGGCACCCGACTCCTCATGGATGATAGCCGAGAACGCC 675
Db 12427 GTGACGATGACCCCGGTTTCGGGATGCGAGCGCTCCTCGACGAGCTTTCGCGCGAGCC 12486
QY 676 GGTTTGTTCCCAATGTGTTTTCGAATCCATGGAACCTCACACCGTGCAGGGTTGTC 735
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Db 12547 GCGCGGGGCTGGATCAGCTGTCGATCGATCGAGCGGAGATCCGTCGGGAGTA 12606
QY 796 ATCGTGCAACGCCCACTTAGTCCACCCGCTTATAGGAACTAGGTTTGGTGTGGCACTC 855
Db 12607 TCCGTCAAGCGCTGCGCGACGCGATGCTACCGCGATGTCGGCATGATCTGGGATCC 12666
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Db 12667 GCGCGCGCTTCCGCGTTTCGCGCGCGCACTTCATCGCGCGCGCGCG 12715

RESULT 15
AF235504/c 77534 bp DNA linear BCT 19-JUL-2000
LOCUS Streptomyces hygroscopicus var. ascomyceticus FK520 biosynthetic
DEFINITION gene cluster, partial sequence.
ACCESSION AF235504
VERSION AF235504.1 GI:9280381
KEYWORDS Streptomyces hygroscopicus subsp. ascomyceticus
SOURCE Streptomyces hygroscopicus subsp. ascomyceticus
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE 1 (bases 1 to 77534)
AUTHORS Wu, K., Chung, L., Revill, W.P., Katz, L. and Reeves, C.D.
TITLE The FK520 gene cluster of Streptomyces hygroscopicus var.
ascomyceticus (ATCC 14891) contains genes for biosynthesis of
unusual polyketide extender units
JOURNAL Gene 251 (1), 81-90 (2000)
MEDLINE 20323220
PUBMED 10863039
REFERENCE 2 (bases 1 to 77534)
AUTHORS Reeves, C.D., Wu, K., Chung, L., Revill, P. and Katz, L.
TITLE Direct Submission
JOURNAL Submitted (16-FEB-2000) Korean Biosciences Inc, 3832 Bay Center
Place, Hayward, CA 94545 USA
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Search completed: April 13, 2005, 01:05:59
Job time : 4175 secs

CC The present sequence is that of the novel *lysR2* gene of *Corynebacterium*
 CC glutamicum strain ATCC 13032. The gene codes for *lysR2* protein (see
 CC AAM51006), a transcriptional regulator of the *lysR* family. The gene was
 CC identified in a cosmid gene library of ATCC 13032 using algorithms and
 CC sequence analysis programs. Vector pCR2.1_{lysR2int}, which carries an
 CC internal fragment (see ABA91927) of the *lysR2* gene, is claimed, and is
 CC deposited in Escherichia coli strain TOP10F/pCR2.1_{lysR2int} as DSM 13617.
 CC Also claimed are coryneform bacteria in which the *lysR2* gene is
 CC attenuated, preferably eliminated, especially by deletion. These bacteria
 CC are used for the production of L-amino acids. Insertional mutagenesis of
 CC the *lysR2* gene in the lysine producer *C. glutamicum* DSM 5715 and the
 CC valine producer *Brevibacterium lactofermentum* FERM BP-1763 using vector
 CC pCR2.1_{lysR2int} improved production of L-lysine and L-valine,
 CC respectively. Further genes of L-amino acid biosynthetic pathways may
 CC also be manipulated. Polynucleotide sequences from the *lysR2* gene may be
 CC used as hybridisation probes, e.g. in arrays, microarrays or DNA chips,
 CC for discovering related sequences

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Query Match 100.0%; Score 930; DB 6; Length 1364;
 Best Local Similarity 100.0%; Pred. No. 3.4e-264;
 Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DT 26-SEP-2001 (first entry)
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 OS organic acid synthesis; ds.
 XX Corynebacterium glutamicum.
 PN EP1108790-A2.
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 PD 20-JUN-2001.
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 PF 18-DEC-2000; 2000EP-00127688.
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 PR 16-DEC-1999; 99JP-00377484.
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 PA (KYOW) KYOWA HAKKO KOGYO KK.
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 PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
 PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
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 DR WPI; 2001-376931/40.
 XX
 PT Novel polynucleotides derived from Coryneform bacteria, for identifying
 PT mutation point of a gene, measuring expression of a gene, analyzing
 PT expression profile or pattern of a gene and identifying homologous gene.
 XX
 PS Disclosure; SEQ ID NO 7069; 246pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of nucleotide and protein
 CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of coryneform bacterium, measuring expression amount and analyzing
 CC the expression profile or expression pattern of a gene derived from
 CC Coryneform bacterium, and identifying a homologue of a gene derived from
 CC Coryneform bacterium. Coryneform bacteria are useful for producing amino
 CC acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a nucleic acid described
 CC in the exemplification of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from the European Patent Office

SQ Sequence 309400 BP; 70133 A; 86477 C; 83115 G; 69675 T; 0 U; 0 Other;

Query Match 100.0%; Score 930; DB 5; Length 309400;
 Best Local Similarity 100.0%; Pred. No. 3.2e-263;
 Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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RESULT 3

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AC AAH68193;

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DT 26-SEP-2001 (first entry)

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XX Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW organic acid synthesis; ds.
XX Corynebacterium glutamicum.
XX EP1108790-A2.
XX 20-JUN-2001.
XX 18-DEC-2000; 2000EP-00127688.
XX 16-DEC-1999; 99JP-00377484.
PR 07-APR-2000; 2000JP-00159162.
PR 03-AUG-2000; 2000JP-00280988.
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX WPI; 2001-376931/40.
DR P-FSDB; AAG92974.
XX Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analyzing
PT expression profile or pattern of a gene and identifying homologous gene.
XX Claim 8; SEQ ID NO 3228; 246pp + Sequence Listing; English.
CC The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and analysing
CC the expression profile or expression pattern of a gene derived from
CC Coryneform bacterium, and identifying a homologue of a gene derived from
CC coryneform bacterium. Coryneform bacteria are useful for producing amino
CC acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the European Patent Office
SQ Sequence 924 BP; 207 A; 286 C; 239 G; 192 T; 0 U; 0 Other;
Query Match 99.4%; Score 924; DB 5; Length 924;
Best Local Similarity 100.0%; Pred. No. 1.7e-262;
Matches 924; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 301 CGACTGGACTTCATGATTCCTTGGGCACTTGGATGGTCCCGAACTTATCCGAACATTC 360
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QY 367 CGCGCGAACACCCCAACGTAGAAATTCACATCCACCAAGCGGACGCAATGCTCTGTGTA 426
DB 361 CGCGCGGAACACCCCAACGTAGAAATTCACATCCACCAAGCGGACGCAATGCTCTGTGTA 420
QY 427 GATCGTGTGTTTGGCTGATGAAGAACTGACCTCGCATTTAGTTGGCCCAAACTCCCGAGGTT 486
DB 421 GATCGTGTGTTTGGCTGATGAAGAACTGACCTCGCATTTAGTTGGCCCAAACTCCCGAGGTT 480
QY 487 GGTACTCTTTAGGTGGCGGCACTGCTTCTGATCAAGCACTTGCCTAGCTGTTCCCGGA 546
DB 481 GGTACTCTTTAGGTGGCGGCACTGCTTCTGATCAAGCACTTGCCTAGCTGTTCCCGGA 540
QY 547 GATCACCCTGCTGCTCTCTTTCTGCGCAAGGAGAAATTCGCTTACTGCGGCGGA 606
DB 541 GATCACCCTGCTGCTCTCTTTCTGCGCAAGGAGAAATTCGCTTACTGCGGCGGA 600
QY 607 GAACCTTTTCGTGGCGATGCGAGCAGGTTTCGGCACCCGACTCTCATGATGATCATTAGCC 666
DB 601 GAACCTTTTCGTGGCGATGCGAGCAGGTTTCGGCACCCGACTCTCATGATGATCATTAGCC 660
QY 667 GAAGAAGCGGTTTGTTCCTCAATGTGTTTTCGAATCCATGGAATCCATGGAATCCATGGA 726
DB 661 GAAGAAGCGGTTTGTTCCTCAATGTGTTTTCGAATCCATGGAATCCATGGAATCCATGGA 720
QY 727 GGGCTTGTGACGCGAGGCTCGGCGTGTGTTGTTCCGATGATGATCCGTTACCTTCCC 786
DB 721 GGGCTTGTGACGCGAGGCTCGGCGTGTGTTGTTCCGATGATGATCCGTTACCTTCCC 780
QY 787 ACAGTGGGAATCGTCAACGCGCCACTTAGTCCACCCGCTTATAGGGAATAGGTTTGGTG 846
DB 781 ACAGTGGGAATCGTCAACGCGCCACTTAGTCCACCCGCTTATAGGGAATAGGTTTGGTG 840
QY 847 TGGGCACTCAACGCGGCGCGCACCTGCGGTGATTAATCTCCGGAAGTTGTTGCGGGA 906
DB 841 TGGGCACTCAACGCGGCGCGCACCTGCGGTGATTAATCTCCGGAAGTTGTTGCGGGA 900
QY 907 TCGAGGTATGATTAAGAGAGGC 930
DB 901 TCGAGGTATGATTAAGAGAGGC 924

RESULT 4

ACA01299
ID ACA01299 standard; DNA; 903 BP.
XX
AC ACA01299;
XX
DT 03-JUN-2003 (first entry)
XX
DE C. glutamicum derived ORF SEQ ID 1290.
XX
KW Coryneform; nucleic acid array; fermentation; culture; ds.
XX
OS Corynebacterium glutamicum.
XX
PN DE10128510-A1.
XX
PD 19-DEC-2002.
XX
PF 13-JUN-2001; 2001DE-01028510.
XX
PR 13-JUN-2001; 2001DE-01028510.
XX
XX (DEGS) DEGUSSA AG.
XX
XX Farwick M, Moeckel B, Pfeifferle W, Bathe B, Huthmacher K;
XX
XX WPI; 2003-279970/28.
XX
XX New nucleic acid array useful for monitoring mRNA expression of
PT Corynebacterium glutamicum during fermentation, comprising nucleic acid
PT from Corynebacterium glutamicum.

XX
PS
XX
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
XX
SQ

Claim 1; Page 457-458; 709pp; German.

This invention describes a novel nucleic acid array involving Corynebacterium glutamicum polynucleotides. The arrays are used to analyse C. glutamicum, particularly for monitoring a fermentation process to determine expression levels of C. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of different strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA0010-ACA02188 represent C. glutamicum derived polynucleotides described in the disclosure of the invention

Sequence 903 BP; 201 A; 281 C; 230 G; 191 T; 0 U; 0 Other;

Query Match 97.1%; Score 903; DB 8; Length 903;

Best Local Similarity 100.0%; Pred. No. 2.7e-256;

Matches 903; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CTGCGAATCGAGCACTACGCGCTTCATTTTCAGTCGCTCAATCAGGCGCACTCACCGAA 87
DB 1 CTGCGAATCGAGCACTACGCGCTTCATTTTCAGTCGCTCAATCAGGCGCACTCACCGAA 60
QY 88 ACTGCGGAAGATTTAGGCATCCCGCAGCCCACTTTCCAGACGAATCAGCGGAGTGAA 147
DB 61 ACTGCGGAAGATTTAGGCATCCCGCAGCCCACTTTCCAGACGAATCAGCGGAGTGAA 120
QY 148 AAAACAGCAGCACTCCCACTTTTCGACGCGCGCGCAAACTCGTCTCAACCAACGA 207
DB 121 AAAACAGCAGCACTCCCACTTTTCGACGCGCGCGCAAACTCGTCTCAACCAACGA 180
QY 208 GGCCACGCTTCTCAACACGCGCGCGCACTTCGCGAGAAATTCAGTCCGCGCACT 267
DB 181 GGCCACGCTTCTCAACACGCGCGCGCACTTCGCGAGAAATTCAGTCCGCGCACT 240
QY 268 GAAATCAAAACGCTTCATGGACCCAGAAAAGGCAAAATCCGACATTCATGCAATCC 327
DB 241 GAAATCAAAACGCTTCATGGACCCAGAAAAGGCAAAATTCGACATTCATGCAATCC 300
QY 328 TTGGGCACTTGGATGGTCCCGCACTTATCCGAACTTCGCGCGCGCAACCCCAACGA 387
DB 301 TTGGGCACTTGGATGGTCCCGCACTTATCCGAACTTCGCGCGCGCAACCCCAACGA 360
QY 388 GAATTCGAATTCACCAAGCGGCGCACTGCTCTGCTAGATCGTGTGTTGGCTGATGA 447
DB 361 GAATTCGAATTCACCAAGCGGCGCACTGCTCTGCTAGATCGTGTGTTGGCTGATGA 420
QY 448 ACTGACCTCGCATTTAGTTGGCCCAAACTTCGCGAGGTTGGTACCTCTTTAGGGTGGCG 507
DB 421 ACTGACCTCGCATTTAGTTGGCCCAAACTTCGCGAGGTTGGTACCTCTTTAGGGTGGCG 480
QY 508 CCACTGCTTCTCAACGACTTGCCTAGCTGTTCCCGCAGATCACCGGCTTGCCTCCTTT 567
DB 481 CCACTGCTTCTCAACGACTTGCCTAGCTGTTCCCGCAGATCACCGGCTTGCCTCCTTT 540
QY 568 TCTGGCAAGAGAAATTTGCGGTTGATTTACTGCGCGGGAAGAACCTTTTCGCGGATGCGA 627
DB 541 TCTGGCAAGAGAAATTTGCGGTTGATTTACTGCGCGGGAAGAACCTTTTCGCGGATGCGA 600
QY 628 GCAGGTTTTCGCGCACCCGACTCTCATGATGCAATAGCCGAAGAGCGGTTTGTGTTCCC 687
DB 601 GCAGGTTTTCGCGCACCCGACTCTCATGATGCAATAGCCGAAGAGCGGTTTGTGTTCCC 660
QY 688 AATGTGTTTTCGAATCCATGGAATCCACCACTGCGAGGCTTGTGAGCGAGGTTCTC 747
DB 661 AATGTGTTTTCGAATCCATGGAATCCACCACTGCGAGGCTTGTGAGCGAGGTTCTC 720
QY 748 GGCCTTGTGTTTTCGATGATGATCCGTTACCTTCCACAGTGGGAATCGTCCACGC 807
DB 721 GGCCTTGTGTTTTCGATGATGATCCGTTACCTTCCACAGTGGGAATCGTCCACGC 780
QY 808 CCACTTAGTCCACCGCTTATAGGGAATAGGTTGTTGGTGGCGACTCAACCGCGGCGCG 867

Db 781 CCACCTTAGTCCACCCGCTTATAGGGAACCTAGGTTGGTGTGGCACTCAACCGGGCGG 840
 QY 868 GCACCTCGCGTGGATAAATTCGCGGAAGTTTCGTGGCGGGATCGAGGTATCGATTAGAGAG 927
 Db 841 GCACCTCGCGTGGATAAATTCGCGGAAGTTTCGTGGCGGGATCGAGGTATCGATTAGAGAG 900
 QY 928 GGC 930
 Db 901 GGC 903

RESULT 5
 ABA91927
 ID ABA91927 standard; DNA; 439 BP.
 XX
 AC ABA91927;
 DT 15-MAY-2002 (first entry)
 XX
 DE Corynebacterium glutamicum lysr2 gene internal fragment.
 KW Lysr2; transcription; regulator; L-amino acid; L-valine; L-lysine;
 KW metabolic engineering; pCR2.1lysR2int; gene; ds.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN WO200212504-A1.
 XX
 PD 14-FEB-2002.
 XX
 PF 15-JUN-2001; 2001WO-BF006808.
 XX
 PR 10-AUG-2000; 2000DE-01039047.
 PR 03-MAR-2001; 2001DE-01010346.
 XX
 XX (DEGS) DEGUSSA AG.
 XX
 PI Moeckel B, Farwick M, Hermann T, Kreutzer C, Pfefferle W;
 XX
 XX WPI; 2002-227155/28.
 XX
 DR Novel lysr2 gene of coryneform bacteria encoding Lysr2 protein which is a
 PT transcription regulator, useful for fermentative production of L-lysine
 PT and L-valine and as a probe detecting polynucleotides encoding Lysr2.
 XX
 PS Example 3; Page 39; 44pp; English.
 XX
 CC The present sequence is that of an internal fragment of the novel lysr2
 CC gene of Corynebacterium glutamicum strain ATCC 13032. The gene fragment
 CC was obtained by PCR amplification of chromosomal DNA using the primers
 CC given in ABA91928 and ABA91929. It was used in the construction of
 CC claimed vector pCR2.1lysR2int, which is deposited in Escherichia coli
 CC TOP10F as DSM 13617. The full-length lysr2 gene (see ABA91926) codes for
 CC Lysr2 protein (see AM51006), a transcription regulator of the lysr
 CC family. The invention provides coryneform bacteria in which the lysr2
 CC gene is attenuated, preferably eliminated, especially by deletion. These
 CC bacteria are used in the production of L-amino acids. In an example of
 CC this, insertional mutagenesis of the lysr2 gene in the lysine producer C.
 CC glutamicum DSM 5715 and in the valine producer Brevibacterium
 CC lactofermentum FERM BP-1763 using pCR2.1lysR2int improved yields of L-
 CC lysine and L-valine, respectively
 XX
 SQ Sequence 439 BP; 100 A; 135 C; 106 G; 98 T; 0 U; 0 Other;

Query Match 47.2%; Score 439; DB 6; Length 439;
 Best Local Similarity 100.0%; Pred. No. 3.3e-119;
 Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 CCATCGTCCGAGAAATTCACCTCGCGCGCAACTCAATCAAAATCAACGCTCATGGACCCAGAAA 295
 Db 1 CCATCGTCCGAGAAATTCACCTCGCGCGCAACTCAATCAAAATCAACGCTCATGGACCCAGAAA 60
 QY 296 AAGGCAATCCGACTGGACTTTCATGCTTCCTTGGGCACTTGGATGGTCCCGAACTTGA 355

Db 61 AAGGCACAATCCGACTGGACTTTCATGCACTTCCTTGGGCACTTGGATGGTCCCGAACTTGA 120
 QY 356 TCCGAACAATTCGCGCGCGCAACACCCCAACGTAAGATTCCCACTCCACCAAGCGGAGCAA 415
 Db 121 TCCGAACAATTCGCGCGCGCAACACCCCAACGTAAGATTCCCACTCCACCAAGCGGAGCAA 180
 QY 416 TGCTCCTCGTAGATCGTGTGTTTGGCTGATGAACACTGACCTCGCAATTAGTTGGCCCCAAC 475
 Db 181 TGCTCCTCGTAGATCGTGTGTTTGGCTGATGAACACTGACCTCGCAATTAGTTGGCCCCAAC 240
 QY 476 CTGCGCAGGTTGGTACCTCTTTAGGTTGGGCGCCACTGCTTCAACGACTTGCCTAG 535
 Db 241 CTGCGCAGGTTGGTACCTCTTTAGGTTGGGCGCCACTGCTTCAACGACTTGCCTAG 300
 QY 536 CTGTTCCCGCAGATCACCGGCTTGGCTCTCTTTCTGGCAAGAGAAATTGCCGTTGATTA 595
 Db 301 CTGTTCCCGCAGATCACCGGCTTGGCTCTCTTTCTGGCAAGAGAAATTGCCGTTGATTA 360
 QY 596 CTGCGCGCGAAGAACCTTTTCGTGGCGATGCGAGCAGGTTTCGGCACCCGACTCCTCATGG 655
 Db 361 CTGCGCGCGAAGAACCTTTTCGTGGCGATGCGAGCAGGTTTCGGCACCCGACTCCTCATGG 420
 QY 656 ATGCATTAGCCGAGAAGC 674
 Db 421 ATGCATTAGCCGAGAAGC 439

RESULT 6
 AAA14651/c
 ID AAA14651 standard; DNA; 77536 BP.
 XX
 AC AAA14651;
 DT 08-AUG-2000 (first entry)
 XX
 DE Nucleotide sequence of the FK-520 biosynthetic gene cluster.
 XX
 KW FK-520; polyketide synthase; PKS; gene cluster; immunosuppressant;
 KW Streptomyces hygroscopicus var. ascomyceticus; immunophilin;
 KW FK-506 binding protein; polyketide compound; transplant rejection;
 KW graft-versus-host disease; uveitis; alopecia universalis;
 KW autoimmune chronic active hepatitis; inflammatory bowel disease;
 KW multiple sclerosis; primary biliary cirrhosis; scleroderma;
 KW neurite outgrowth; nerve regrowth; Parkinson's disease;
 KW Alzheimer's disease; stroke; traumatic spinal cord; brain injury;
 KW peripheral neuropathy; ss.
 XX
 OS Streptomyces hygroscopicus.
 XX
 FH Key Location/Qualifiers
 CDS complement(412..1836)
 FT /tag= a
 FT /note= "fkBW gene"
 FT complement(2020..3579)
 FT /tag= b
 FT /note= "fkBV gene"
 FT 3969..4496
 FT /tag= c
 FT /note= "fkBR2 gene"
 FT complement(4595..5488)
 FT /tag= d
 FT /note= "fkBR1 gene"
 FT 5601..6818
 FT /tag= e
 FT /note= "fkBE gene"
 FT 6808..8052
 FT /tag= f
 FT /note= "fkBF gene"
 FT 8156..8824
 FT /tag= g
 FT /note= "fkBG gene"
 FT complement(9122..9883)

```

FT      CDS      /tag= h
FT      /note= "fkfH gene"
FT      complement(9894..10994)
FT      /tag= i
FT      /note= "fkfI gene"
FT      complement(10987..11247)
FT      /tag= j
FT      /note= "fkfJ gene"
FT      complement(11244..12092)
FT      /tag= k
FT      /note= "fkfK gene"
FT      complement(12113..13150)
FT      /tag= l
FT      /note= "fkfL gene"
FT      complement(13212..23988)
FT      /tag= m
FT      /note= "fkfC gene"
FT      complement(13452..13662)
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FT      /tag= q
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FT      complement(16587..17820)
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FT      /note= "acyltransferase domain (AT) 6"
FT      complement(17820..19053)
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FT      /tag= u
FT      /note= "KRS"
FT      complement(20241..21420)
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FT      /tag= w
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FT      complement(22653..23892)
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FT      52362..53576
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FT      /tag= bc
FT      /note= "ER7"
FT      56943..57575
FT      /tag= bd
FT      /note= "KR7"
FT      57710..57920

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FT      /*tag= be
FT      /note= "ACP7"
FT      misc_feature 5790..59243
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FT      /note= "KS8"
FT      misc_feature 59244..60398
FT      /*tag= bg
FT      /note= "AT8"
FT      misc_feature 60399..61412
FT      /*tag= bh
FT      /note= "DH8 (inactive)"

Query Match      14.1%; Score 131.2; DB 3; Length 77536;
Best Local Similarity 50.8%; Pred. No. 2.9e-27;
Matches 375; Conservative 0; Mismatches 348; Indels 15; Gaps 2;

QY      27  CTTGCGAATCGACGACCTTACGAGCTTATTTTCAGTCGCTCAATCAGGCCACCTCACCGA 86
Db      |||
Db      5489 CATGGAGATACGGAGTTCAGTGGTTACGGCTTGGCGGACGACGACGACGATGACGAT 5430
QY      87  AACTGCCGAAAGATTAGGCATCCGCGACGCCACATTTCCAGACGAATCAGCCGAGTGGA 146
Db      |||
Db      5429 CACCGCGGAACGGCTCAACATCTCCAGCGACCTGTCCAGGGCCATCCGGGGCTGA 5370
QY      147 AAAACACGCGAGCACCCCACTTTTCGACCGCGCGCGCAAACTGCTCTCAACCAACG 206
Db      |||
Db      5369 GCGACGAGTGGCGTCCGCTGTTCGACCGGGACAGAACCGCTCCGGCTCAACAAGTA 5310
QY      207 AGCCAGGCTTCTCAACACGCGAGCGCATCTGCGCAGAAATTCATCTCGCGCGCAAC 266
Db      |||
Db      5309 CGCGAGGCTTTCGCGCGCCACGCTTCCGCGCGATCAGTGAAGTCTCCGCGCGCGAGCA 5250
QY      267 TGAATCAAAAGCCTCATGGACCCAGAAAAGSCAAATCCGACTGCTTCATGCTATTC 326
Db      |||
Db      5249 GCGCATACGCGCTGATGACACCCGACACCGGACCGTGGACATGGTTTCTGCACTC 5190
QY      327 CTTGGCACTTGGATGTTCCCGAACTTATTCGAAATTCGCGCGCGCAACACCCCAACGT 386
Db      |||
Db      5189 CTACGGCACTGGCTGTGCGGACCTCTCTGCGGGTACCGCGGCTCCCGGCAC 5130
QY      387 AGAATTCGAATCCACGAGCGGACGAATGCTCTGCTGATGATCGTGTTCGCTGATGA 446
Db      |||
Db      5129 CACCTTCGAACCTGCGCGGCGAGCGCCCGACGCGCTGGTCGACGAGCTCCGCAACAGCAG 5070
QY      447 AACTGACCTCGCATTAGTTGGCCCAACCTGCGAGGTTGTTACCTCTTTAGGGTGGGC 506
Db      |||
Db      5069 GCTGGACCTGGGCTGACAGCCCAACGACCCCGCGGG-----ACGATGTGAGTGGAC 5016
QY      507 GCACCTGCTTCTGTCACGACTTGGCCCTAGTGTGTTCCCGCAGATCACCGGCTTGCCTCTT 566
Db      |||
Db      5015 ACCACTGCGGACGAGGCACTGTGCTGCTGCTCCCAACCGGACACCGGCTGGCC----- 4961
QY      567 TTCGCGCAAGGAGAAATGCGTTGATTAATCTGCGCGGGAAGAACCTTCTGTCGCGATGCG 626
Db      |||
Db      4960 ----AGACGCGCGCGGTGGGACCGCGGAGCTGGCGGATGAGCGCTTCGTGGCACTGA 4905
QY      627 AGCAGGTTTCGCGACCCGACTCTCATGATGATGATAGCCGAGAGCGGTTTGTTC 686
Db      |||
Db      4904 GCGGGTCTTCGGAATCCAGATACCGACCGGCTGTGCGCGCGCGGATTCGTGCT 4845
QY      687 CAATGTGGTTTTCGAATCCATGGAATCAACCACTGCGCAGGCGCTTGTGAGCGCAGGCT 746
Db      |||
Db      4844 GCGGGTCTTCGGAATCCAGATACCGACCGGCTGTGCGCGCGCGGATTCGTGCT 4785
QY      747 CGCGGTTGTGTGGTTCC 764
Db      |||
Db      4784 CGGTGTGGCGGTGCGCCC 4767

RESULT 7
ABD13720
ID      ABD13720 standard; DNA; 927 BP.
XX

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```

AC      ABD13720;
XX
XX      29-JUL-2004 (first entry)
XX
XX      Pseudomonas aeruginosa polynucleotide #12324.
XX
XX      Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW      antibacterial.
XX
XX      Pseudomonas aeruginosa.
XX
XX      US6551795-B1.
XX
XX      22-APR-2003.
XX
XX      18-FEB-1999; 99US-00252991.
XX
XX      18-FEB-1998; 98US-0074788P.
XX
XX      27-JUL-1998; 98US-0094190P.
XX
XX      (GENO-) GENOME THERAPEUTICS CORP.
XX
XX      Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
XX      WPI; 2003-615309/58.
XX
XX      P-PSDB; ABO80149.
XX
XX      Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT      useful as molecular targets for diagnostics, prophylaxis and treatment of
PT      pathological conditions resulting from bacterial infection.
XX
XX      Disclosure; SEQ ID NO 12324; 455pp; English.
XX
XX      The invention relates to Pseudomonas aeruginosa polypeptides and the
CC      polynucleotides encoding them. The sequences are useful in diagnosis and
CC      therapy of pathological conditions, as molecular targets for diagnostics,
CC      prophylaxis and treatment of pathological conditions resulting from a
CC      bacterial infection, for evaluating a compound, such as a polypeptide,
CC      for the ability to bind a P. aeruginosa nucleic acid, as components of
CC      effective antibacterial targets, as targets for antibacterial drugs,
CC      including anti-P. aeruginosa drugs, as templates for recombinant
CC      production of P. aeruginosa-derived peptides or polypeptides, as target
CC      components for diagnosis and/or treatment of P. aeruginosa-caused
CC      infection, and in detection of P. aeruginosa sequences or other sequences
CC      of Pseudomonas species using biochip technology. Sequences ABD01397-
CC      ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC      The sequence data for this patent did not form part of the printed
CC      specification but was obtained in electronic format from USPTO at
CC      seqdata.uspto.gov/sequence.html
XX
XX      Sequence 927 BP; 161 A; 355 C; 279 G; 132 T; 0 U; 0 Other;

Query Match      7.3%; Score 68; DB 11; Length 927;
Best Local Similarity 49.2%; Pred. No. 2.3e-09;
Matches 179; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

QY      38  ACGACCTACGACGCTTCAATTCAGTCGCTCAATCAGGCCACCTCACCGAACTGCCGAAA 97
Db      |||
Db      44  ACAGCTCAACACCTTCATCGCCATTCGCGAGACCGGAGCTTCTCGAAGCGGGGAGC 103
QY      98  GATTAGGATCCCGCAGCCACACATTTCCAGACGAATCAGCGAGTGGAAAACACGACG 157
Db      |||
Db      104  GCCTGACCTGACCCCAACCGGGGTGAGCAAGCGCATCCGCCCTCGAACAGCAGCTCA 163
QY      158  GCACCCGCTTTTCACCGCGCGCGCGCAAACTGCTCTCAACCAACGAGGCGCGCT 217
Db      |||
Db      164  ATGCCCGGCTGTTCGACCGGGTCCGCGCGAGGTCAACCTCACCGAGCGCGCGGCC 223
QY      218  TCCTCAACCCAGCGCGGCTATCGTCGCGAGAAATCAACTCCGCCGCACTGAAATCAAA 277
Db      |||
Db      224  TGCTGCGCGCGGCTTACAGTGTGCTCAACGTCGACGACACCCCGCGGGGCTGTGAACA 283
QY      278  GCCTCATGACCCAGAAAAGGCAATCCGACTGGACTTCATGCTTCCTTTGGGACATT 337

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Db 284 ACCTACCGCGAGGTCACGCGCGGCTGCTCTGGCCACACGACACATCGCGCTGC 343
 Qy 338 GGATGGTCCCGAATTATCCGAACATTCGCGCGCGAAGACACCCCAAGTAGAATTCACAC 397
 Db 344 ATCGCTGCGCGCGCTGCTGCGCGCTTACCGCGCGCATCCGCGAGGTGGCGCTGGATA 403
 Qy 398 TCCA 401
 Db 404 TCCA 407

RESULT 8
 ABD13492/c
 ID ABD13492 standard; DNA; 972 BP.
 XX
 AC ABD13492;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Pseudomonas aeruginosa polynucleotide #12096.
 XX
 KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
 KW antibacterial.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN US6551795-B1.
 XX
 PD 22-APR-2003.
 XX
 PF 18-FEB-1999; 99US-00252991.
 XX
 PR 18-FEB-1998; 98US-0074788P.
 PR 27-JUL-1998; 98US-0094190P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX
 DR WPI; 2003-615309/58.
 DR P-PSDB; ABO79921.
 XX
 PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 12096; 455pp; English.
 XX
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences ABD01397-
 CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 972 BP; 141 A; 287 C; 368 G; 176 T; 0 U; 0 Other;
 Query Match 7.3%; Score 68; DB 11; Length 972;
 Best Local Similarity 49.2%; Pred. No. 2.3e-09;
 Matches 179; Conservative 0; Mismatches 185; Indels 0; Gaps 0;
 Qy 38 ACGACTACGAGCTTCATTTTCAGTCGCTCAATCAGCGCACCTCACCGAAATCGCGAAA 97

Db 890 ACAGCTCAACACCTTTCATCCCATTCGCGAGACCGGAGCTTCTCCGAAGCCGCGAGC 831
 Qy 98 GATTAGGATCCCGAGCCACACATTTCCAGACGAATCAGCCGAGTGGAAAAACACGAG 157
 Db 830 GCCTGCACCTGACCAACCGCGGCTGAGCAAGCGCATCGCGCGCTCCGAACAGAGCTCA 771
 Qy 158 GCACCCCACTTTTCGACGCGCGCGCGGCGCAAACTCGTCTCAACGACGAGGCGACGCT 217
 Db 770 ATGCCCGCTGTTTCGACCGGCTCGCGCGCGAGGTCAACTCACGAGCGCGCGCGCCC 711
 Qy 218 TCCTCAACACGCGCGCGCATTCGTCGAGAAATTCAACTCCGCGCGCAACTGAAATCAAAC 277
 Db 710 TGCTCCCGCGCTTACAGTTGCTCAACGCTGCTCGACGACACCGCGCGGCTGACACA 651
 Qy 278 GCCTCATGGACCCAGAAAAAGGCAATCCGACTGGACTTCATGCAATTCCTTGGGCACTT 337
 Db 650 ACCTCACCGCGAGGTGAGCGCGGCTGCTGCTGGCCACCGACACCATCGGCTGC 591
 Qy 338 GGATGGTCCCGAACTTATCCGACATTCGCGCGCGGACACCCCACTAGATTCACAC 397
 Db 590 ATCGCTGCGCGCGCTGCTGCGCGCTTACC CGGCGCATCCGAGGTGGCTGGATA 531
 Qy 398 TCCA 401
 Db 530 TCCA 527

RESULT 9
 ABD13817
 ID ABD13817 standard; DNA; 1482 BP.
 XX
 AC ABD13817;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Pseudomonas aeruginosa polynucleotide #12421.
 XX
 KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
 KW antibacterial.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN US6551795-B1.
 XX
 PD 22-APR-2003.
 XX
 PF 18-FEB-1999; 99US-00252991.
 XX
 PR 18-FEB-1998; 98US-0074788P.
 PR 27-JUL-1998; 98US-0094190P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX
 DR WPI; 2003-615309/58.
 DR P-PSDB; ABO80246.
 XX
 PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 12421; 455pp; English.
 XX
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant

CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1482 BP; 269 A; 555 C; 431 G; 227 T; 0 U; 0 Other;
Query Match 7.3%; Score 68; DB 11; Length 1482;
Best Local Similarity 49.2%; Pred. No. 2.7e-09;
Matches 179; Conservative 0; Mismatches 185; Indels 0; Gaps 0;
QY 38 ACGACCTACGCGAGCTTCATTTCAGTCGCTCAATCAGGCGCACCTCACCAGAACTGCGGAAA 97
DB 99 ACAGCCTCAACACTTCATCGCATTGCGAGACCGGAGCTTCCTCGAAGCGGGAGC 158
QY 98 GATTAGGATCCCGCAGCCACACATTTCCAGACGAATCAGCGAGTGGAAAAACACGCGAG 157
DB 159 GCGTCACCTGACCCAAACCGCGGTGAGCAAGCGCATCGCCCTCGAACACGAGCTCA 218
QY 158 GCACCCCATTTTGAACCGCGCGCGGCAAACTGTCTCTCAACCAACGAGGCGCAGCCT 217
DB 219 ATGCCCGGCTGTTCGACCGGCTCGCGCGGAGTCAACCTCACCAGGCGCGCGCGCC 278
QY 218 TCTCAACACCGCGCGGCGCATGTCGCGAGATTCAACTCCCGCGCACTGAATCAAC 277
DB 279 TGTGCGCGCGCTTACCGAGTTGCTCAACGTCTCGACGACACCGCGCGGCGCTGAACA 338
QY 278 GCTCATGACCGCAGAAAAAGGACAAATCCGACTGACCTTCATGCTTCCTTTGGGCACTT 337
DB 339 ACTCACCGCGAGGTTCAGCGCGCGGTGCTCTGCGCACAGCCACACATCGCGCTGC 398
QY 338 GGATGCTCCCGAATTATCCGAACATTCGCGCGCGAAACACCCCAACGTTAGAAATCCAAC 397
DB 399 ATCGCTGCGCGCGCTGCTGCGCGCTTCACCGCGCGCATCCGCGAGTGGCGCTGGATA 458
QY 398 TCCA 401
DB 459 TCCA 462

RESULT 10
ABD08478
ID ABD08478 standard; DNA; 987 BP.
AC ABD08478;
XX
XX 29-JUL-2004 (first entry)
XX
XX Pseudomonas aeruginosa polynucleotide #7082.
XX
XX Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
XX antibacterial.
XX
XX Pseudomonas aeruginosa.
XX
XX US6551795-B1.
XX
XX 22-APR-2003.
XX
XX 18-FEB-1999; 99US-00252991.
XX
XX 18-FEB-1998; 98US-0074788P.
XX
XX 27-JUL-1998; 98US-0094190P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX WPI; 2003-615309/58.
XX

DR P-PSDB; AB074907.
XX
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX useful as molecular targets for diagnostics, prophylaxis and treatment of
XX pathological conditions resulting from bacterial infection.
XX
XX Disclosure; SEQ ID NO 7082; 455pp; English.
XX
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
XX polynucleotides encoding them. The sequences are useful in diagnosis and
XX therapy of pathological conditions, as molecular targets for diagnostics,
XX prophylaxis and treatment of pathological conditions resulting from a
XX bacterial infection, for evaluating a compound, such as a polypeptide,
XX for the ability to bind a P. aeruginosa nucleic acid, as components of
XX effective antibacterial targets, as targets for antibacterial drugs,
XX including anti-P. aeruginosa drugs, as templates for recombinant
XX production of P. aeruginosa-derived peptides or polypeptides, as target
XX components for diagnosis and/or treatment of P. aeruginosa-caused
XX infection, and in detection of P. aeruginosa sequences or other sequences
XX of Pseudomonas species using biochip technology. Sequences ABD01397-
XX ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
XX The sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html
SQ Sequence 987 BP; 189 A; 352 C; 298 G; 148 T; 0 U; 0 Other;
Query Match 6.6%; Score 61.4; DB 11; Length 987;
Best Local Similarity 47.7%; Pred. No. 2.1e-07;
Matches 179; Conservative 0; Mismatches 196; Indels 0; Gaps 0;
QY 27 COTCGGAATCGACGACCTACGCGAGCTTCATTTTCAGTCGCTCAATCAGGCGCACCTCACCGA 86
DB 78 CTTGCGTTTCGAGGATATCGAAGCTTCTCTCAACGTGCGCGAACTCAACAGCGTGAGGTC 137
QY 87 AACTGCCGAAGATTAGGATATCCCGAGCCCACTTTTCAGACGAATCAGCGGAGTGGA 146
DB 138 GCGCGCGGAGCGCATGAGCCTGTCCAAGTGGTGATCAGCAAGCGTGTGAGGATCTCGA 197
QY 147 AAAACACGCGGCGACCCCACTTTTCGACGCGCGCGCGCAAACTCGTCTCAACCAACG 206
DB 198 ACGAGCGCTCGCGCTGCTCTATCGACACGCGCGCAACGTCGAGCGCACCGAGCG 257
QY 207 AGGCCACGCGCTTCTCTCAACACGCGCGCGCGCATCTCGCAGAAATTCATTCGCGCGCAAC 266
DB 258 CGGCGATTCTTCTACAGGCGCGCAAGCGCTCGCTGCGAGGAATCAACACGCGCGGA 317
QY 267 TGAATCAAAACGCTCATGAGACCCAGAAAAAGGCAATTCGACTGGAGTTCATGATTC 326
DB 318 GATTGTCGCGCTGCGGAGAACGACCTGTGCGCGAAATTCGCGCATCGTCAACCCGATGAG 377
QY 327 CTTGGCGACTTGGATGTTCCCGGAATTCATCGAACATTCGCGCGGCAACCCCAACCT 386
DB 378 CTTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 437
QY 387 AGAAATCCCACTCCA 401
DB 438 GGAGATCGTCTGCA 452
RESULT 11
ABD08454
ID ABD08454 standard; DNA; 1485 BP.
XX
XX ABD08454;
XX
XX 29-JUL-2004 (first entry)
XX
XX Pseudomonas aeruginosa polynucleotide #7058.
XX
XX Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
XX antibacterial.
XX


```
OS Pseudomonas aeruginosa.
XX US6551795-B1.
XX 22-APR-2003.
XX 18-FEB-1999; 99US-00252991.
XX 18-FEB-1998; 98US-0074788P.
XX 27-JUL-1998; 98US-0094190P.
XX (GENO-) GENOME THERAPEUTICS CORP.
XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX WPI; 2003-615309/58.
XX P-PSDB; ABO74883.
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX useful as molecular targets for diagnostics, prophylaxis and treatment of
XX pathological conditions resulting from bacterial infection.
XX Disclosure; SEQ ID NO 7058; 455pp; English.
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
XX polynucleotides encoding them. The sequences are useful in diagnosis and
XX therapy of pathological conditions, as molecular targets for diagnostics,
XX prophylaxis and treatment of pathological conditions resulting from a
XX bacterial infection, for evaluating a compound, such as a polypeptide,
XX for the ability to bind a P. aeruginosa nucleic acid, as components of
XX effective antibacterial targets, as targets for antibacterial drugs,
XX including anti-P. aeruginosa drugs, as templates for recombinant
XX production of P. aeruginosa-derived peptides or polypeptides, as target
XX components for diagnosis and/or treatment of P. aeruginosa-caused
XX infection, and in detection of P. aeruginosa sequences or other sequences
XX of Pseudomonas species using biochip technology. Sequences ABD01397-
XX ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
XX The sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html
XX
XX Sequence 1485 BP; 297 A; 531 C; 443 G; 214 T; 0 U; 0 Other;
XX
Query Match 6.6%; Score 61.4; DB 11; Length 1485;
Best Local Similarity 47.7%; Pred. No. 2.5e-07;
Matches 179; Conservative 0; Mismatches 196; Indels 0; Gaps 0;
QY 27 CCTGCGAATCGACGACCTACGAGCTTTCATTTTCAGTCGCTCAATCAGGCCACCTCACCGA 86
DB 124 CTGCGTTTCGACGATATCGAGCTTCTCAACGTCGCCGNACTCAACAGGTGACGTC 183
QY 87 AACTGCCGAAGATTAGGATCCCGAGCCACACTTTCCAGACGAATCAGCCGAGTGGGA 146
DB 184 GCGCGCCGAGCGCATGAGCTGTCCAAAGTCGGTGATCAGCAAGCGTGTCAAGCATCTGA 243
QY 147 AAAACACGACGACGCCACCTTTTCGACGCGCGCGCGCAACTCGTCTCAACACAG 206
DB 244 AGACGCTCTGGCGTCCGCTCTCTATCGACACGCGCGCAAGTCGAGCGGACCGAGGC 303
QY 207 AGGCCACGCTCTCTCAACACGCGCGGCCATCTGTCGAGAAATTCACACTCGCGCGCAAC 266
DB 304 CGGCGATTCTTCTACAGGCGCGCAAGGCTCGTGCAGGNACTCAACAGCGCGCGGA 363
QY 267 TGAATCAACGCTCTATGGACCCAGAAAAGGACAAATCGCACTGGACATTCATCATTC 326
DB 364 GATTGTGCGCTCTGCGGAGACGACCTGTGCGCGGAATTTGGCATCTGTCACTCATGAG 423
QY 327 CTTGGGCACTTGGATGGTCCCGAATCTATCGACATTTCCGCGCGGACACCCCAAGT 386
DB 424 CTTGCGGACCTCTGCTGTGCTCCGATCATCGCGGACTTATGAGCCAGCACCCGCGCT 483
QY 387 AGAATTCCAACTCCA 401
XX
Db 484 GGAGATCGTCTCTGCA 498
RESULT 12
ABD08440/c
XX ABD08440 standard; DNA; 1518 BP.
XX AC ABD08440;
XX DT 29-JUL-2004 (first entry)
XX DE Pseudomonas aeruginosa polynucleotide #7044.
XX KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
XX antibacterial.
XX OS Pseudomonas aeruginosa.
XX PN US6551795-B1.
XX PD 22-APR-2003.
XX PF 18-FEB-1999; 99US-00252991.
XX PR 18-FEB-1998; 98US-0074788P.
XX PR 27-JUL-1998; 98US-0094190P.
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX WPI; 2003-615309/58.
XX P-PSDB; ABO74869.
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX useful as molecular targets for diagnostics, prophylaxis and treatment of
XX pathological conditions resulting from bacterial infection.
XX Disclosure; SEQ ID NO 7044; 455pp; English.
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
XX polynucleotides encoding them. The sequences are useful in diagnosis and
XX therapy of pathological conditions, as molecular targets for diagnostics,
XX prophylaxis and treatment of pathological conditions resulting from a
XX bacterial infection, for evaluating a compound, such as a polypeptide,
XX for the ability to bind a P. aeruginosa nucleic acid, as components of
XX effective antibacterial targets, as targets for antibacterial drugs,
XX including anti-P. aeruginosa drugs, as templates for recombinant
XX production of P. aeruginosa-derived peptides or polypeptides, as target
XX components for diagnosis and/or treatment of P. aeruginosa-caused
XX infection, and in detection of P. aeruginosa sequences or other sequences
XX of Pseudomonas species using biochip technology. Sequences ABD01397-
XX ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
XX The sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html
XX
XX Sequence 1518 BP; 213 A; 451 C; 554 G; 300 T; 0 U; 0 Other;
XX
Query Match 6.6%; Score 61.4; DB 11; Length 1518;
Best Local Similarity 47.7%; Pred. No. 2.5e-07;
Matches 179; Conservative 0; Mismatches 196; Indels 0; Gaps 0;
QY 27 CCTGCGAATCGACGACCTACGAGCTTTCATTTTCAGTCGCTCAATCAGGCCACCTCACCGA 86
DB 1429 CCTGCGTTTCGACGATATCGAAGCTTCTCAACGTCGCCGNACTCAACAGGTGACGTC 1370
QY 87 AACTGCCGAAGATTAGGATCCCGAGCCACACTTTCCAGACGAATCAGCCGAGTGGGA 146
DB 1369 GCGCGCGGAGCGCATGAGCTGTCCAAAGTCGGTGATCAGCAAGCGTGTCAAGCATCTGA 1310
QY 147 AAAACACGACGACGCCACCTTTTCGACGCGCGCGCGCAACTCGTCTCAACACCAACG 206
```

Db 1309 ACAGCGCTCGGCTCGCTCTATCCACACCGCGCAACGTCGAGCCGACGAGGC 1250
Qy 207 AGCCACGCTTCTCAACACCGCCAGCGCATCTGCGAGAAATTCAACTCCGCCGCAAC 266
Db 1249 CGGGCATTTCTTACAAAGCGCCCAAGGCTCGCTGCGAGAACTCAACAACGCCGCGGA 1190
Qy 267 TGAATCAACGCTCATGACCAAGCAAGAAAGCAATCCGACTGACTTCATGATTC 326
Db 1189 GATTTGTCGCCCTCGCGGAGAACACCTGTGCGCGCAATTGCGCATGCTCACCCCGATGAG 1130
Qy 327 CTGGGCACTTGGATGTCCTCCGAACTTATCCGAACATTCGCGCGCAACACCCCAACCT 386
Db 1129 CTTGCGACCTCTGCTGTCGCGGATCATCGCGCACTTATGAGCAGACCCGCGCT 1070
Qy 387 AGAATTCCAACTCCA 401
Db 1069 GGAGATCGTCTGCA 1055

RESULT 13

ACA43570

ID ACA43570 standard; DNA; 891 BP.

AC ACA43570;

XX

DT 19-JUN-2003 (first entry)

XX Prokaryotic essential gene #25227.

XX

KW Antisense; ds; prokaryotic essential gene; cell proliferation;

KW drug design; gene.

XX

OS Pseudomonas putida.

XX

XX WO200277183-A2.

XX

XX 03-OCT-2002.

XX

XX 21-MAR-2002; 2002WO-US009107.

XX

XX 21-MAR-2001; 2001US-00815242.

XX

XX 06-SEP-2001; 2001US-00948993.

XX

XX 25-OCT-2001; 2001US-0342923P.

XX

XX 08-FEB-2002; 2002US-00072851.

XX

XX 06-MAR-2002; 2002US-0362699P.

XX

XX (ELIT-) ELITRA PHARM INC.

XX

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX

XX WPI; 2003-029926/02.

XX

XX P-PSDB; ABU39700.

XX

PS Claim 14; SEQ ID NO 31440; 1766pp; English.

XX

CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of

CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 891 BP; 163 A; 294 C; 270 G; 164 T; 0 U; 0 Other;

Query Match

Best Local Similarity 6.5%; Score 60; DB 8; Length 891;

Matches 195; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

Qy 38 ACGACCTACGCGAGCTTTCATTTTCAGTCGCTCAATCAGGCCACCTCACCGAAATTCGCCAAA 97

Db 17 AGACATCAGATCTTTTCGTGAATAATCGCGAATCTGGGAGTTTCATAGGGCGCCGAAG 76

Qy 98 GATTAGGATCCCGCAGCCACATTTCCAGACGAATCAGCCGAGTGGAAAAACACGACAG 157

Db 77 CGCTCCACTTTGTCAGCGCGCCCTGAGCCGAGGATCAAGAAGCTGGAGGAAGGCTCG 136

Qy 158 GCACCCCTTTTCGACCGCGCGCGCAAACTCGTCTCAACCAACGAGGCGCAGCCT 217

Db 137 GCACCTCGCTACTGGAACGCACTCGCGGGTTCAGCTCAGCGTGGGCGCGGACT 196

Qy 218 TCCTCAACACGCGAGCGCATCTGTCGAGAAATTCACCTCGCGCCCACTGAAATCAAC 277

Db 197 TCCTGCCAAGCCAGCGCGCTGCTGGATGATTTTGAAGACTCGATCTCAGCATCCGCG 256

Qy 278 GCCTCATGAGCCAGAAAAAGCACAATCCGACTGGACTTCATGATTCCTTTGGGACATT 337

Db 257 AGCTGGCGAGCGCCAGACCGGTACGTTACCTCGCTGCAATCTCTACCGCGGCTTCT 316

Qy 338 GGATGGTCCCGAATTCGGAACATTCGCGCGCGCAACACCCCAACGTAGAATTCGAAC 397

Db 317 ACTTCTCGCTGCGGTGATTCGCGGATTAACAGAGCAATACCCGAAATTCGCAATTCGCG 376

Qy 398 TCACCAAGCGCGCAGCAATGCTCTGCTGATAGTCTGTTTGGCTGATGAACCTGACCTCG 457

Db 377 TGCTGGACCTTAGCGCCCAACGACGCGCTCGAAGCCGCTGCGCGGCGGCGGACTTCG 436

RESULT 14

AAH68525/c

ID AAH68525 standard; DNA; 349980 BP.

XX AC AAH68525;

XX

XX 26-SEP-2001 (first entry)

XX

XX C glutamicum coding sequence fragment SEQ ID NO: 7060.

XX

XX Corynebacterium; amino acid synthesis; vitamin; saccharide;

XX

XX organic acid synthesis; ds.

XX

XX Corynebacterium glutamicum.

XX

XX EP1108790-A2.

XX

XX 20-JUN-2001.

XX

PF 18-DEC-2000; 2000EP-00127688.
XX
PR 16-DEC-1999; 93JP-00377484.
PR 07-APR-2000; 2000JP-00159162.
PR 03-AUG-2000; 2000JP-00280988.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
XX WPI; 2001-376931/40.
XX
XX Novel polynucleotides derived from Corynebacterium bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analyzing
PT expression profile or pattern of a gene and identifying homologous gene.
XX
XX Disclosure; SEQ ID NO 7060; 246pp + Sequence Listing; English.
XX
XX The present invention provides a number of nucleotide and protein
CC sequences from the Corynebacterium bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of corynebacterium, measuring expression amount and analyzing
CC the expression profile or expression pattern of a gene derived from
CC Corynebacterium bacterium, and identifying a homologue of a gene derived from
CC Corynebacterium bacterium. Corynebacterium bacteria are useful for producing amino
CC acids, nucleic acids, vitamins, saccharides and organic acids, described
CC particularly L-lysine. The present sequence is a nucleic acid, described
CC in the exemplification of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the European Patent Office
XX
SQ Sequence 349980 BP; 80289 A; 91081 C; 97378 G; 81232 T; 0 U; 0 Other;

Query Match 6.5%; Score 60; DB 5; Length 349980;
Best Local Similarity 51.5%; Pred. No. 6.2e-06;
Matches 138; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

QY 22 GGAGACCTGGGAATCGACGACCTACGACGCTTCATTTCAGTCGCTCAATCAGCGCCACCTC 81
Db 142488 GCACACATGCGACCTCAATCAGCTCGAATTTTTCATCGCAGTAGGCCAACACGGACGATC 142429

QY 82 ACCGAAATCTGCGAAAGATTAGGCATCCGCGAGCCACACTTTCAGACGCAATCAGCCGA 141
Db 142428 AACCGCGCGCGAGAGACTCTCTCATTTCCCAACCGCTCTCAGCGCAGATCTCCGA 142369

QY 142 GTGGAATAACAGCGAGGACCCACTTTTCGACGCGCGCGCGCAAACTCGTCTCAAC 201
Db 142368 CTTGAAAAATCGTCGGAGCTCCACTTTCGAAACGCCATTCGCGGGTGTCTCCCTACA 142309

QY 202 CAACGAGGCGACGCTTCTCAACACGCGCGCCATCGTCGAGAAATCAACTCCGCC 261
Db 142308 AGGCGGAGAAATCTTCACGAGAGCCCTTCGAAAGCTTAGCAGGATGCAATCGGTA 142249

QY 262 GCAACTGAAATCAAAACGCTCATGACC 289
Db 142248 GTCGATGAAATCAATCCGGTGAGCAC 142221

RESULT 15
ACA26845
ID ACA26845 standard; DNA; 954 BP.
XX
XX ACA26845;
AC
XX
XX 19-JUN-2003 (first entry)
DT
XX
XX Prokaryotic essential gene #8502.
DE
XX
XX Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
XX Bordetella pertussis.

XX WO200277183-A2.
PN
XX
PD 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
PF
XX
XX 21-MAR-2001; 2001US-00815242.
PR
XX 06-SEP-2001; 2001US-00948993.
PR
XX 25-OCT-2001; 2001US-0342923P.
PR
XX 08-FEB-2002; 2002US-00072851.
PR
XX 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
PI
XX
XX WPI; 2003-029926/02.
DR
XX P-PSDB; ABU22975.
DR
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 14; SEQ ID NO 14715; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
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SQ Sequence 954 BP; 149 A; 350 C; 302 G; 153 T; 0 U; 0 Other;

Query Match 6.4%; Score 59.8; DB 8; Length 954;
Best Local Similarity 47.5%; Pred. No. 6.1e-07;
Matches 178; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

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Db 16 GATCTGTCCACCCCGCAATTCGCGCCTTCGCTCATGCTTGCACCTCGCGCACTTACC 75

QY 85 GAAACTGCCGAAGATTAGGCATCCGCGAGCCCACTTTCCAGACGCAATCAGCCGAGTG 144
Db 76 AAGCGCGCGAGGATGCAATTTGTCACGCCCGCATTCAGGCACTGATCCAGTCCCTG 135

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Db      |||
QY 205 CGAGGCCACGCTTTCCTCAACACGCGCAGCGCCATCGTCGCAGAATTCAACTCCGCGCGCA 264
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Db      |||
QY 265 ACTGAAATCAAAACGCTTCATGGACCCAGAAAAAGGCACAAATCCGACTGGACTTTCATGCAT 324
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QY 256 ACCACATCGCCAGCTTCGTGAGTTGCGGCGCGGGCGGTCCATGTGCGCGCCCTTCCC 315
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QY 325 TCCTTGGGCACTTGGATGCTCCCGAACTTATCCGAAACATTCGCGCGCGAAACACCCCAAC 384
Db      |||
QY 316 TCCCTGGCGCGGGATGCTGCGGAAAGTCTCTGATGAGTTCCACGCGGAGACCCCGGAC 375
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QY 385 GTAGATTCCACTC 399
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Job time : 583 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 23:13:05 ; Search time 3101 Seconds
(without alignments)

11415.598 Million cell updates/sec

Title: US-09-826-909-1_COPY_232_1161

Perfect score: 930

Sequence: 1 gtagcattgggcaacgacgg.....ggtagtcattagaagagggc 930

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

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6: gb_est5:*

7: gb_est6:*

8: gb_gsa1:*

9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67.4	7.2	760	9	CC842306
2	57.8	6.2	766	8	BZ573361
3	57.8	6.2	847	8	BZ553158
4	57.8	6.2	1350	8	BZ554839
5	57.6	6.2	1175	8	BZ568637
6	57.4	6.2	990	8	BZ573643
7	56.8	6.1	1077	8	BZ563333
8	56.2	6.0	717	7	CN822018
9	56.2	6.0	768	7	CN822012
10	56.2	6.0	853	7	CO202977
11	55.8	6.0	850	8	BZ424306
12	55.6	6.0	817	8	BZ566287
13	55.2	5.9	674	8	AZ9333780
14	55	5.9	1072	8	BZ579898
15	54.8	5.9	451	8	BZ422864
16	54.6	5.9	800	7	CF933278
17	54.4	5.8	1161	8	BZ556936
18	54.2	5.8	391	9	P294R
19	53.4	5.7	780	8	BZ560257
20	53.2	5.7	1106	8	BZ559233
21	53	5.7	722	8	AZ933651
22	52.8	5.7	551	1	A1409183
23	52	5.6	815	7	CN822455
24	52	5.6	820	7	CO202387

25	51	5.5	721	8	BZ562255	BZ562255
26	50.4	5.4	729	7	CN822500	CN822500
27	50.2	5.4	331	2	BF291112	BF291112
28	50.2	5.4	806	8	BZ551243	BZ551243
29	50.2	5.4	1291	8	BZ568924	BZ568924
30	50	5.4	734	8	AY080301	AY080301
31	49.2	5.3	1013	8	BZ548324	BZ548324
32	48.8	5.2	1212	8	BZ579976	BZ579976
33	47.6	5.1	673	8	BZ548565	BZ548565
34	47.4	5.1	1327	8	BZ571615	BZ571615
35	47	5.1	406	7	CO000903	CO000903
36	46.6	5.0	1280	8	BZ578104	BZ578104
37	46.2	5.0	636	8	BH190115	BH190115
38	46.2	5.0	922	9	CNS0073W	AL066784
39	46.2	5.0	1512	8	BZ557409	Drosophil
40	46.2	5.0	2328	9	CL982230	pac81-60
41	46	4.9	884	9	CNS006U0	CL982230
42	46	4.9	909	9	CNS000JTL	OaIFSC047
43	46	4.9	1052	8	BZ559123	Drosophil
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ALIGNMENTS

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LOCUS ND.L105A23.T7 Notre Dame Liverpool Aedes aegypti genomic clone
DEFINITION CC842306
ACCESSION CC842306
VERSION CC842306.1 GI:33188999
KEYWORDS GSS:
SOURCE Aedes aegypti (yellow fever mosquito)
ORGANISM Aedes aegypti
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
Stegomyia.
REFERENCE 1 (bases 1 to 760)
AUTHORS Lofus,B., Shetty,J., Knudson,D. and Severson,D.
TITLE BAC end sequencing of Aedes aegypti
JOURNAL Unpublished (2003)
COMMENT Other GSSs: ND.L105A23.SP6
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
Library was provided by David Severson
Seq primer: 17
Class: BAC ends.

FEATURES
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Best Local Similarity 50.4%; Pred.No. 5.9e-08;
Matches 192; Conservative 0; Mismatches 186; Indels 3; Gaps 1;
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Db 3 CTTTACCCGCGCGGGAATAAATCTTTCGTCAACCAGCCACCATCAGCAAGATGCTCGG 62
 Qy 138 CCGAGTGAATAACAGCAGGACCCCACTTTTCGACCGCGCGCGCCCAACTGCTCT 197
 Db 63 GCATCTGGAAGAGGAGCTGGAATGACACGCTGCTGATCCGCGAAGCGCGCAAGCTGCGCT 122
 Qy 198 CAACCAACGAGCGCAGCTTCTCTCAACAGCAGCGCCATCGTCGAGAAATCAACTC 257
 Db 123 GACCGACAGCGCGCAGCGGTGTATCAGCGCGGCTGACGATCTCGAGAAATCCGCA 182
 Qy 258 CGCCGCAACTGAATCAACGCGCTCATGAGCCAGAAAAGGACCAATCCGACTGACTT 317
 Db 183 GCTGAGCGGAGCTGGAAGACATCAGCTCGTGTGAAAAGGCGTGTGCGCTGGCAT 242
 Qy 318 CATGATCTCTTGGCACTTGATGCTCCGCAATTCGCAATTCGCGCGCAACA 377
 Db 243 TCCGCGGATGTTGGGCA---GCGAGATCGCGATCTGATCGCGCTTTTCGCGAGACCTA 299
 Qy 378 CCCCAACGTAGAATTCCAACTCCACCAAGCGCAGCAATGCTCTGCTAGATCGGTGTTT 437
 Db 300 CCCCGGATCGAATTAATAATTCGAGCTGGCGGCTGTGCTGCGAAGCGGTGAT 359
 Qy 438 GCGTGATGAATGACCTCGC 458
 Db 360 GTCCGCGAAGTGGATCTGGC 380

RESULT 2
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 LOCUS msh2_307.x3 msh Pseudomonas aeruginosa genomic clone msh2_307, 766 bp DNA linear GSS 17-DEC-2002
 DEFINITION genomic survey sequence.

ACCESSION BZ573361
 VERSION BZ573361.1 GI:27208422
 KEYWORDS GSS.

SOURCE Pseudomonas aeruginosa
 ORGANISM Pseudomonas aeruginosa
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.

REFERENCE 1 (bases 1 to 766)
 AUTHORS Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
 TITLE Whole-Genome-Sequence variation among multiple isolates of Pseudomonas aeruginosa library
 JOURNAL J. Bacteriol. (2002) In press
 COMMENT Contact: Chris K. Raymond
 Genome Center
 University of Washington
 Box 352145, Seattle, WA 98105-2145, USA
 Tel: 2062216954
 Fax: 2066857244
 Email: craymond@u.washington.edu
 Class: shotgun.

FEATURES
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 Location/Qualifiers
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 /mol_type="Genomic DNA"
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 Matches 125; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

Qy 27 CTTGGAATCGACGACCTAGCAGCTTCATTTTCAGTCGCTCAATCAGGCGACCTCACCGA 86
 Db 301 CTTGCGCTTTGAAGACATACAGGCTTCCTCAACGTGTCGAGCTGGGCGAGCATCAGCGC 360

Qy 87 AACTGCCGAAAGATTAGGCATCCCGCAGCCACACTTTTCCAGAGCAATCAGCCGAGTGA 146
 Db 361 CGCGCGGAGCGCATGAGCTGTCAAGTCGTGATCAGCAAAACGCTCAGGACCTGA 420
 Qy 147 AAAACAGCAGCAGGACCCCACTTTTCGACCGCGCGCGCAAACTCGTCTCAACCAACG 206
 Db 421 CGGCCACCTCGGCTGCGCTGTCTACCGCTCGACGCGCAACGTCGAGCGCGACCGAGGC 480
 Qy 207 AGGCACGCTTCTCAACAGCGCGCGCATCGTCGAGAAATCAACTCGCGCGC 263
 Db 481 CGCGGCTTCTTCTACAAAGTCGCGCAAGGCTCGCTGCAGGACCTGAACAACGCGCGC 537

RESULT 3

BZ553158/c

LOCUS

DEFINITION BZ553158 847 bp DNA linear GSS 17-DEC-2002
 pacsl-60_4007.y2 pacsl-60 Pseudomonas aeruginosa genomic clone
 pacsl-60_4007, genomic survey sequence.

ACCESSION BZ553158
 VERSION BZ553158.1 GI:27158829
 KEYWORDS GSS.

SOURCE Pseudomonas aeruginosa
 ORGANISM Pseudomonas aeruginosa

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
 1 (bases 1 to 847)

REFERENCE 1 (bases 1 to 847)
 AUTHORS Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.

TITLE Whole-Genome-Sequence variation among multiple isolates of Pseudomonas aeruginosa library
 JOURNAL J. Bacteriol. (2002) In press

COMMENT Contact: Chris K. Raymond
 Genome Center
 University of Washington
 Box 352145, Seattle, WA 98105-2145, USA
 Tel: 2062216954
 Fax: 2066857244
 Email: craymond@u.washington.edu
 Class: shotgun.

FEATURES
 source

Location/Qualifiers
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Qy 27 CTTGGAATCGACGACCTAGCAGCTTCATTTTCAGTCGCTCAATCAGGCGACCTCACCGA 86
 Db 408 CTTGCGCTTTGAAGACATACAGGCTTCCTCAACGTGTCGAGCTGGGCGAGCATCAGCGC 349
 Qy 87 AACTGCCGAAAGATTAGGCATCCCGCAGCCACACTTTTCCAGAGCAATCAGCCGAGTGA 146
 Db 348 CGCGCGGAGCGCATGAGCTGTCCAAGTCGTGATCAGCAAAACGCTCAGGACCTGA 289
 Qy 147 AAAACAGCAGGACCCCACTTTTCGACCGCGCGCGCAAACTCGTCTCAACCAACG 206
 Db 288 CGGCCACCTCGGCGTGTGCGCTGTCTACCGCTCGACGCGCAACGTCGAGCGCGAGGC 229
 Qy 207 AGGCACGCTTCTCAACAGCGCGCGCATCGTCGAGAAATTCAACTCGCGCGC 263
 Db 228 CGCGGCTTCTTCTACAAAGTCGCGCAAGGCTCGCTGCAGGACCTGAACAACGCGCGC 172


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RESULT 4
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LOCUS
DEFINITION
pac61-60_4884.x1 pac61-60 Pseudomonas aeruginosa genomic clone
pac61-60_4884, genomic survey sequence.
ACCESSION
BZ554839
VERSION
BZ554839.1 GI:27162898
KEYWORDS
GSS.
SOURCE
Pseudomonas aeruginosa
ORGANISM
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
REFERENCE
1 (bases 1 to 1350)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol. (2002) In press
JOURNAL
Pseudomonas aeruginosa library
COMMENT
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
FEATURES
Location/Qualifiers
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QY 27 CTGCGAATCGACGACCTACGAGCTTCATTTTCAGTCGCTCAATCAGGCACTCACC6A 86
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Db 242 CTGCGCTTGAAGACATACAGCCCTTCTCAACGTGTCGAGCTGGCGAGCATCAGCGC 301
QY 87 AACTCGCGAAGATTAGGATCCCGAGCCACACTTTCCAGACGAATCAGCCGAGTGA 146
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QY 147 AAACACGCGAGCACCCCACTTTTCGACGCGCGCGCAAACTCGTCTCAACCAAG 206
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Db 362 GCGCACCTCGCGGTGGCGCTCTTACCGCTCGAGCGCAACGTCGAGCCGACGAGGC 421
QY 207 AGGCCACGCTTCTCTCAACACGCGAGCCCACTCGTCGAGAAATCAACTCGCGCGC 263
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LOCUS
DEFINITION
pac62-164_766.s3 pac62-164 Pseudomonas aeruginosa genomic clone
pac62-164_766, genomic survey sequence.
ACCESSION
BZ568637
VERSION
BZ568637.1 GI:27201914
KEYWORDS
GSS.
SOURCE
Pseudomonas aeruginosa
ORGANISM
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
REFERENCE
1 (bases 1 to 1175)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol. (2002) In press
JOURNAL
Pseudomonas aeruginosa library
COMMENT
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
FEATURES
Location/Qualifiers
1..1175
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QY 219 CCTCAACACGCGCGCGCATGTCGCGAGATTCAACTCCGCGCGCACTGAATCAACG 278
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QY 339 GATGTCCTCCGAACTTATCCGAACATTCGCGCGCGAACCACCCCAACGTAGAAATTCAC 398
Db 219 TCTGTACCGCGCATACTCAGAGCGTTCGCGCAACAGCATGGCGCTGCCAGCT 160
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Db 159 CCAGGAAG 152

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msh2_3292.x1 msh Pseudomonas aeruginosa genomic clone msh2_3292,
genomic survey sequence.
ACCESSION
BZ573643
VERSION
BZ573643.1 GI:27208704
KEYWORDS
GSS.
SOURCE
Pseudomonas aeruginosa
ORGANISM
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
REFERENCE
1 (bases 1 to 990)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol. (2002) In press
JOURNAL
Pseudomonas aeruginosa library
COMMENT
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
FEATURES
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QY 219 CCTCAACACGCGCGCGCATGTCGCGAGATTCAACTCCGCGCGCACTGAATCAACG 278
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QY 399 CCACCAAG 406
Db 159 CCAGGAAG 152

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JOURNAL
COMMENT
Pseudomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.

FEATURES

source
Location/Qualifiers
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QY 35 TCGACGACTAGCGAGCTTCAATTCAGTCGCTCAATCAGGCACCTCACCAGAACTGCCG 94
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QY 95 AAAGATTAGGATCCCGCAGCCACACTTTCAGACGAATCAGCGAGTGGAAACACG 154
DB 318 AGGACTGGGACACCCAGCTCGGTGACGACGAGATCAAGCTTGAGAAAGAGC 377
QY 155 CAGCACCCTCTTTTCAGCCGCGCGCCGCAAACTCGTCTCAACCAACGAGGCCACG 214
DB 378 TGGCACCCTCTGTTCAGCGCGTTTCATCAGGCGATCGTCTCAGCAGCGCGCCAGC 437
QY 215 CTTTCTCAACGCGCAGCGCATCTGTCGAGAGATTCACCTCGCC 261
DB 438 TTCTGCTCCGCACGTGGCGCGCGCCTCGAGACGATCGATGCCGCG 484

RESULT 7
BZ563333
LOCUS
DEFINITION
pac2-164_4204.y2 pac2-164 Pseudomonas aeruginosa genomic clone
pac2-164_4204, genomic survey sequence.
ACCESSION
VERSION
BZ563333.1 GI:27186978
KEYWORDS
SOURCE
ORGANISM
Pseudomonas aeruginosa
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
REFERENCE
1 (bases 1 to 1077)
AUTHORS
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
TITLE
Whole-Genome-Sequence Variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol. (2002) In press
JOURNAL
COMMENT
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.

FEATURES

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/organism="Pseudomonas aeruginosa"
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/clone_lib="pac2-164"
/note="Clinical isolate 2-164 Whole genomic shotgun library."

ORIGIN

Query Match 6.1%; Score 56.8; DB 8; Length 1077;
Best Local Similarity 46.0%; Pred. No. 7e-05;
Matches 190; Conservative 0; Mismatches 223; Indels 0; Gaps 0;

QY 39 CGACTACGAGCTTCAATTCAGTCGCTCAATCAGGCACCTCACCAGAACTGCCGAAAG 98
DB 144 CCAACTCGCTATTTTCGTCGCTCTACGAGAGGCCACGTCGCGCGCGCGCGAAACG 203
QY 99 ATTAGGCATCCCGCAGCCACACTTTCAGACGAATCAGCGAGTGGAAAAACACGACGAG 158
DB 204 CTTGCCCTGTGCAACCGGCCCTCTCGACGAGATCGCCAGTTGGAGCAGACCTCGA 263
QY 159 CACCCCACTTTTCAGCCGCGCGCGCAAACTCGTCTCAACCAACGAGGCCAGCCTT 218
DB 264 CGTCTCGCTGTTCAGCGCGCAGCGCAAGCGCTGTGCGCACCTGCGCGCCACACCT 323
QY 219 CTTCAACACGCGCAGCGCATCTGTCGAGAAATTCAACTCCGCCCACTGAAATCAACG 278
DB 324 GTACACCATTCGGGTACCGTCTGAGGAGATTGGAAGGGCCCGGAGGCGATCGCGGT 383
QY 279 CCTCATGACCCAGAAAGGCACAAATCCGACTGCACTTCATGATTCCTTTGGGCACTTG 338
DB 384 ATTCCGGGGCAGACCCCGCGCAGCTGGCGATCGGCTACTGCAGCGGTCAAGCCAG 443
QY 339 GATGTCCTCCGAATTCGGAACATTCGCGCGCGCAACACCCCAACGAGTAGAATTCCAACT 398
DB 444 CTTGTCGCTGTATGTCGAAACGCTGCACGCGTCGACCGCATGTCGGGTGCAGAT 503
QY 399 CCACCAAGCGCACAATGCTCTGGTAGATCGGTTTGGCTGATGAACTG 451
DB 504 CTACGAATGTCGGAAATGACATCGAGCGCGCGCTGCTCACCAGGAACCTG 556

RESULT 8

CN822018 717 bp mRNA linear EST 02-JUN-2004
LOCUS
DEFINITION
Oa_splbn_10N24_M13reverse Sheep spleen\brain psporti library Ovis
aries cDNA clone Oa_splbn_10N24 5', mRNA sequence.
ACCESSION
VERSION
CN822018.1 GI:47950087
KEYWORDS
SOURCE
Ovis aries (sheep)
Ovis aries
REFERENCE
1 (bases 1 to 717)
AUTHORS
Goessner, A. and Hopkins, J.
TITLE
Ovine spleen\brain cDNA library
JOURNAL
COMMENT
Unpublished (2004)
Contact: J Hopkins
Veterinary Biomedical Sciences
University of Edinburgh
Summerhall Square, Edinburgh, EH9 1QH.
Email: j.hopkins@ed.ac.uk
Plate: 10 row: N column: 24
Seq primer: M13reverse
High quality sequence start: 6
High quality sequence stop: 550.
FEATURES
Location/Qualifiers
1..717
/organism="Ovis aries"
/mol_type="mRNA"
/db_xref="taxon:9940"
/clone="Oa_splbn_10N24"

Db 438 ACACCTCGGTACGCGCTGTTTATCCGCGCGAGCGAGCTAGCCTGACCGAGCGG 497
 Qy 209 GCACGCGCTTCTCAACACGCGCGGATCGTGCAGAAATTCAACTCCGCGCAATG 268
 Db 498 GCGCGCATTTGTTATCGAGGAGGCGACCGCTGCGGAGTTTCAGTTTCCCGCAGCA 557
 Qy 269 AAATCAAAAGCGCTCATGACCCAGAAAAGGCACAAATCCGACTGCACTTCATGATTCCT 328
 Db 558 ATGCCAGCGCGCGGCGGTGAGATTGGTTCACATTTGGGTACGTTGCGTCGG 617
 Qy 329 TGGGCACCTT 337
 Db 618 CGGTCTATT 626

RESULT 11
 BZ424306/c
 LOCUS BZ424306 550 bp DNA linear GSS 10-DEC-2002
 DEFINITION id59d05.g1 WGS-SbicolorF (DH5a methyl filtered) Sorghum bicolor
 genomic clone id59d05 5', genomic survey sequence.

ACCESSION BZ424306
 VERSION BZ424306.1 GI:26374408
 KEYWORDS GSS.
 SOURCE Sorghum bicolor (sorghum)

ORGANISM Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE 1 (bases 1 to 550)

AUTHORS Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N.,

Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,

Zutavern,T., Palmer,I., McCombie,W.R. and Martienssen,R.A.

Genomic shotgun sequences from Sorghum bicolor (methyl-filtered)

Unpublished (2002)

CONTACT: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Plate: id59 row: d column: 05

Seq primer: -21M13UnivRev

Class: shotgun

High quality sequence stop: 560.

FEATURES

Location/Qualifiers

1..550

/organism="Sorghum bicolor"

/mol_type="genomic DNA"

/db_xref="taxon:4558"

/clone="id59d05"

/lab_host="DH5a"

/clone_lib="WGS-SbicolorF (DH5a methyl filtered)"

/note="Site 1: Xba I; Site 2: Xba I; The vector was

digested with XbaI and one nucleotide was added by fill in

in the recessive 3' end. The genomic DNA was nebulized,

and repaired, adaptor ligated and size fractionated using

sephadex. The resulting fragments were between 0.8 and 3

kb and were cloned into the vector (.x/y reads in M13mp19,

.b/g reads in pUC19). The same ligation was transformed

into DH5a."

ORIGIN

Query Match 6.0%; Score 55.8; DB 8; Length 550;

Best Local Similarity 52.9%; Pred. No. 0.00012;

Matches 120; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

Qy 16 GACGCGGAGACCTCGGATCGACGACCTAGCAGCTTCATTTCAGTCGCTCAATCAGGC 75

Db 501 GACGTTTGTATATGAACTTCGCACCTGGTATTTCGTTCGCGTTGCTGAAACGAG 442

Qy 76 CACCTCACCGAACTGCCGAAAGATTAGGCATCCGCGAGCCACACTTTCAGAGCAATC 135

Db 441 CACTTACCCGCGCGCGAGTTCTGGCATGTGCGAGCCACCGCTCAGCCAGCAATC 382
 Qy 136 AGCCAGTGGAAAAACAGCAGGACCCCACTTTTCGACCGCGCGCGCAAACTCGTC 195
 Db 381 CAGCGGCTGGAGCAGCAGATCGGCACGCGCTTGTGAGCGCCTGACGCGCGCGTGGAA 322
 Qy 196 CTCAACCAACAGCGCCGCGCTTCTCAACACCGCAGCGCCATCGT 242
 Db 321 CTGACCGGATCGGCGCGCGCTTCTGCCGATGCAATAGCGATTGT 275

RESULT 12

BZ566287

LOCUS BZ566287

DEFINITION

pac82-164_6003.y2 pacs2-164 Pseudomonas aeruginosa genomic clone

pac82-164_6003, genomic survey sequence.

ACCESSION BZ566287

VERSION BZ566287.1 GI:27195555

KEYWORDS GSS.

SOURCE Pseudomonas aeruginosa

ORGANISM Pseudomonas aeruginosa

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

Pseudomonadaceae; Pseudomonas.

REFERENCE 1 (bases 1 to 817)

AUTHORS Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,

Burns,J.L., Kaul,R. and Olsen,M.V.

Whole-Genome-Sequence variation among multiple isolates of

Pseudomonas aeruginosa library

J. Bacteriol. (2002) In press

CONTACT: Chris K. Raymond

Genome Center

University of Washington

Box 352145, Seattle, WA 98105-2145, USA

Tel: 2062216954

Fax: 2066857244

Email: craymond@u.washington.edu

Class: shotgun

FEATURES

Location/Qualifiers

1..817

/organism="Pseudomonas aeruginosa"

/mol_type="genomic DNA"

/strain="2-164"

/db_xref="taxon:287"

/clone="pac82-164_6003"

/clone_lib="pacs2-164"

/note="clinical isolate 2-164 Whole genomic shotgun

library."

ORIGIN

Query Match

Best Local Similarity

Matches 161; Conservative

0; Mismatches 154; Indels

3; Gaps 1;

Qy 89 CTGCCGAAAGATTAGGCATCCCGCAGCCACACATTTCCAGACGAATCAGCCAGTGGAAA 148

Db 125 CCGTGTAGCGCTGCATGCGCCAGCCACCGCTGACCATCGCATCGCGCGGTGGAG 184

Qy 149 AACACGAGGACCCCACTTTTCGACCGCGCGCGCAAACTCGTCTCAACCAACGAG 208

Db 185 AAGAAGTGGCGGCGAGCTGTGGAGCGTGACACCGTATCCACCGCTGACGCGGCGAG 244

Qy 209 GCACGCGCTTCTCAACACGCGCAGCGCATCGTGGAGAAATTCATCCCGCGCAATG 268

Db 245 GCGCGCGCTTCTCGACGAAGCCCGCGCGCACCTTGGGCCAGCGCAACCTGGCGG 304

Qy 269 AAATCAAAAGCGCTCATGACCCAGAAAAGGCACAAATCCCGACTGACTTCATGATTCCT 328

Db 305 ---CCGCGGAGCGCGCCAGCGGAGCGAGAACTTGGCGCTGGCGTTCGTCCAGCA 361

Qy 329 TGGGCACTTGATGGTCCCGAACTTATCCGAACTTATCCGCGCGGAAACACCCCAACGAG 388

Db 362 CCATCAATATTCTGTCTACCGCGCATACTCCAGGGGTTCCGCAACAGCATGGCGGCTGG 421

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QY 389 AATTCAATCCACCAAG 406
Db 422 ACTTCAGCTCCAGGAAG 439

RESULT 13
AZ933780
LOCUS DEFINITION 674 bp DNA linear GSS 24-APR-2001
Bj_Ba001B08r B. japonicum BAC library Bradyrhizobium japonicum
genomic, genomic survey sequence.
ACCESSION AZ933780
VERSION AZ933780.1 GI:13775840
KEYWORDS GSS.
SOURCE Bradyrhizobium japonicum
ORGANISM Bradyrhizobium japonicum
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
REFERENCE 1 (bases 1 to 674)
AUTHORS Tomkins,J.P., Wood,T.C., Stacey,M.G., Loh,J.T., Judd,A.,
Goicoechea,J.L., Stacey,G., Sadowsky,M.J. and Wing,R.A.
TITLE A marker-dense, sequence-ready map of the Bradyrhizobium japonicum
genome
JOURNAL Genome Res. 11 (8), 1434-1440 (2001)
MEDLINE 21376150
PUBMED 11483585
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Class: BAC ends
High quality sequence stop: 621.

FEATURES
source
location/Qualifiers
1..674
/organism="Bradyrhizobium japonicum"
/mol_type="genomic DNA"
/strain="USD110"
/db_xref="taxon:375"
/lab_host="B. coll"
/clone_lib="B. japonicum BAC library"
/note="Vector: pIndigo536; Site 1: HindIII"

ORIGIN
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Best Local Similarity 49.1%; Pred. No. 0.00018;
Matches 144; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

QY 41 ACCTACGCAGCTTCATTTTCAGTCGCTCAATCAGGCCACCTCACCGAAACTGCCGAAAGAT 100
Db 334 AGCTCAGGACCTTCAGTTGCGTGGCGGAGCTCGGAGCTCTCCAAAGGGTCCGACAGC 393
QY 101 TAGGCATCCCGCAGCCCACTTTTCAGACGAATCAGCGAGTGGAAACACACGAGCA 160
Db 394 TCGCGGTGGCGCAGCGCGGCTCAGCGCGCAGATCAAGCTTCTGGAACACGAGTGGCA 453
QY 161 CCCCACTTTTCAGCGCGCGCGCAAACTGCTCTCAACCAACGAGGCCAGCCTTCC 220
Db 454 TCGAACTGTTCAGCGGCAACGCTCGCGGATGCTGACCGAGCCGCGGCTTCTGC 513
QY 221 TCAACGAGCCAGCGCCATCGTCGAGAAATCAACTCCGCGCAACTGAATCAACAGCC 280
Db 514 TCGCAGGACCTCCGGCATCTGTCGGCAGATCGACAGATCGCGACGACATCCAGTCGG 573
QY 281 TCATGACCCAGAAAAAGCACAATCCGACTGGAATTCATGCAATTCCTTGGGC 333
Db 574 CCAAGGGGCGGCGTCCGCGCAGGTGCTGTTGGCTGTTGGCTGTTCCGACCGTGAGC 626

RESULT 14
BZ579898
LOCUS DEFINITION 1072 bp DNA linear GSS 17-DEC-2002
msh2 832.Y2 msh Pseudomonas aeruginosa genomic clone msh2_832,
genomic survey sequence.
ACCESSION BZ579898
VERSION BZ579898.1 GI:27214959
KEYWORDS GSS.
SOURCE Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
REFERENCE 1 (bases 1 to 1072)
AUTHORS Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
Burns,J.L., Kaul,R. and Olsen,M.V.
TITLE Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
JOURNAL J. Bacteriol. (2002) In press
COMMENT Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: Shotgun.

FEATURES
source
location/Qualifiers
1..1072
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="MSH"
/db_xref="taxon:287"
/clone_lib="msh2_832"
/clone_lib="msh"
/note="Environmental isolate. Whole genomic shotgun
library."

ORIGIN
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Best Local Similarity 52.4%; Pred. No. 0.00023;
Matches 121; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

QY 38 AGCACTACGCAGCTTCATTTTCAGTCGCTCAATCAGGCCACCTCACCGAAACTGCCGAAA 97
Db 272 ACAGCTCAACACCTTCATCGCCATTCGCGAGACCGGAGCTTCTCCGAAGCCGCGAGC 331
QY 98 GATTAGGCATCCGCGAGCCACACTTTCAGACGAATCAGCGAGTGGAAACACGCGAG 157
Db 332 GCCTGCACCTGACCAACCGGGGTGAGCAAGCGATCGCCGCTCTCGAACAGCAGCTCA 391
QY 158 GCACCCCACTTTTCAGCCGCGCGCAAACTGCTCTCAACCAACGAGGCCAGCCT 217
Db 392 ATGCCCGCTGTTCGACCGGGTTCGCGCGAGGTCAACTCACCGAGCCGCGCGCCC 451
QY 218 TCCTCAACACGCGAGCCCATTCGTCGAGAAATCAACTCCGCGCACTG 268
Db 452 TGCTGCCGCGCCCTACCAATTGCTTAAGCTGCTCGAGCAGACCCCGCGCG 502

RESULT 15
BZ422864
LOCUS DEFINITION 451 bp DNA linear GSS 10-DEC-2002
ids9d05.b1 WGS-SbicolorF (DH5a methyl filtered) Sorghum bicolor
genomic clone ids9d05 5', genomic survey sequence.
ACCESSION BZ422864
VERSION BZ422864.1 GI:26371550
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 451)
AUTHORS Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N.,
Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,

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Search completed: April 13, 2005, 01:59:27
Job time : 3109 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 23:32:55 ; Search time 206 Seconds
(without alignments)

7387.075 Million cell updates/sec

Title: US-09-826-909-1_COPY_232_1161

Perfect score: 930

Sequence: 1 gtgaccatgggcaacgacgg.....ggatgcattagaagagggc 930

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:**

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- 2: /cgn2.6/prodata/1/ina/5B COMB.seq:**
- 3: /cgn2.6/prodata/1/ina/6A COMB.seq:**
- 4: /cgn2.6/prodata/1/ina/6B COMB.seq:**
- 5: /cgn2.6/prodata/1/ina/PCUS COMB.seq:**
- 6: /cgn2.6/prodata/1/ina/backfiles1.seq:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	129.6	13.9	77536	4	US-09-410-551B-1
C 2	129.6	13.9	77536	4	US-09-940-316B-1
C 3	68	7.3	927	4	US-09-252-991A-12324
C 4	68	7.3	972	4	US-09-252-991A-12096
C 5	68	7.3	1482	4	US-09-252-991A-12421
C 6	61.4	6.6	987	4	US-09-252-991A-7082
C 7	61.4	6.6	1485	4	US-09-252-991A-7058
C 8	61.4	6.6	1518	4	US-09-252-991A-7044
C 9	59.2	6.4	1035	4	US-09-252-991A-13904
C 10	57.8	6.2	657	4	US-09-252-991A-3008
C 11	57.8	6.2	1074	4	US-09-252-991A-2667
C 12	57.4	6.2	471	4	US-09-252-991A-5341
C 13	57.4	6.2	552	4	US-09-252-991A-5279
C 14	57.4	6.2	909	4	US-09-252-991A-5304
C 15	57.4	6.2	2592	4	US-09-252-991A-5260
C 16	56.4	6.1	771	4	US-09-252-991A-3268
C 17	56.4	6.1	888	4	US-09-252-991A-3414
C 18	56.4	6.1	1197	4	US-09-252-991A-3336
C 19	55	5.9	7295	4	US-09-902-540-924
C 20	54.8	5.9	711	4	US-09-252-991A-12330
C 21	54.8	5.9	930	4	US-09-252-991A-12091
C 22	54.6	5.9	19394	4	US-09-902-540-1172
C 23	54.2	5.8	945	4	US-09-252-991A-2028
C 24	54.2	5.8	984	4	US-09-252-991A-3477
C 25	54.2	5.8	1392	4	US-09-252-991A-3486
C 26	54	5.8	921	4	US-09-252-991A-3438
C 27	54	5.8	1263	4	US-09-252-991A-3462

28	53.8	5.8	885	4	US-09-902-540-8724	Sequence 8724, Ap
29	53.6	5.8	891	4	US-09-902-540-3768	Sequence 3768, Ap
30	53.6	5.8	936	4	US-09-902-540-3745	Sequence 3745, Ap
31	53.6	5.8	17897	4	US-09-902-540-1182	Sequence 1182, Ap
C 32	53.6	5.8	20303	4	US-09-902-540-1183	Sequence 1183, Ap
33	53.4	5.7	936	4	US-09-489-039A-2270	Sequence 2270, Ap
34	53.2	5.7	732	4	US-09-252-991A-6298	Sequence 6298, Ap
C 35	53.2	5.7	855	4	US-09-252-991A-11951	Sequence 11951, A
36	53.2	5.7	897	4	US-09-489-039A-1429	Sequence 1429, Ap
C 37	53.2	5.7	945	4	US-09-252-991A-6167	Sequence 6167, Ap
38	53.2	5.7	978	4	US-09-252-991A-12061	Sequence 12061, A
39	53.2	5.7	1602	4	US-09-252-991A-6382	Sequence 6382, Ap
40	53	5.7	621	4	US-09-252-991A-1463	Sequence 1463, Ap
C 41	53	5.7	939	4	US-09-252-991A-1511	Sequence 1511, Ap
42	53	5.7	3429	4	US-09-252-991A-1663	Sequence 1663, Ap
C 43	52.6	5.7	936	4	US-09-252-991A-12221	Sequence 12221, A
44	52.4	5.6	948	4	US-09-252-991A-12230	Sequence 12230, A
45	52	5.6	291	4	US-09-252-991A-6225	Sequence 6225, Ap

ALIGNMENTS

RESULT 1
US-09-410-551B-1/c
; Sequence 1, Application US/09410551B
; Patent No. 6503737
; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTI, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
; FILE REFERENCE: 30062-20026.00
; CURRENT APPLICATION NUMBER: US/09/410,551B
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 77536
; TYPE: DNA
; ORGANISM: Streptomyces hygroscopicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52275)...(71465)
US-09-410-551B-1

Qy	27	CCTCGGAATCGACGACCTACGAGCTTCATTTTCAGTCGCTCAATCAGGCCACCTCACCGA	86
Db	5489	CATGAGATACGGAGTTGCACTGTTTACGGCTTGGCCGACGACGACGTCGACGAT	5430
Qy	87	AACTCCGGAAGATTAGGATCCCGAGCCCACTTTCCAGACGATCAGCGGAGTGA	146
Db	5429	CACCGGGAACGGCTCAACATCTCCAGCCGACCTGTCTCAGGCGCATCCGCGGCTGA	5370
Qy	147	AAACACGACGACCAACCCACTTTTCGACGCGCGCGGCAAACTGCTCTCAACCAACG	206
Db	5369	GGCAGTAGTGGCGGTGCGCTTTGACCGGCACAGAACCGGCTCCGGCTCAACAGTA	5310
Qy	207	AGGCCACGCTTCTCTCAACACGACGCGCCATCGTCGAGAAATTCACCTCGCGCAAC	266

Db 5309 CGCGAGGTTCTTCGCGGCCACCGCCCTGCGCGCATCTAGTGGTCTCCGCGCCGAGCA 5250
Qy 267 TGAATCAACCGCTCATGAGCAGCAGAAAGCAATCCAGCTGGACTTTCATGATTC 326
Db 5249 GCGCATACCGCCCTGATGACCCCGACACCGGACCGTGGCACTGGGTTTCTGCACTC 5190
Qy 327 CTTGGCACTTGATGGTCCCGAACTTATCCGAATTCGCGCGCAACCCCAAGT 386
Db 5189 CTAGGCACTGGTGGTGGCCGACCTCTCGCGGTTACCGCGGCTGGCTCCCGGCAC 5130
Qy 387 AGAATTCGAATCCCAAGCGCGCAGCAATGCTCTGTGTAGATCGTGTTCGCTGATGA 446
Db 5129 CACCTTCGAATCGCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5070
Qy 447 AACTGACCTCGCATAGTTAGTTGGCCCAACCTCGCGAGGTGTGATCTTTAGGGTGGC 506
Db 5069 GCTGACCTCGGGCTGACAGCCCAACGACCGCGCGG-----ACGATGTGGAGTGGAC 5016
Qy 507 GCACCTGCTTCGTCACGACTTGCCTAGCTGTCCCGCAGATCACCGGCTTGCCTT 566
Db 5015 ACACCTGCGGACGAGGCACTGTGCTGTCTGCTCCACCGGACACCGGCTGGCC----- 4961
Qy 567 TTCTGCGCAAGAGAAATTCGCGTGAATTAATCTCGCGGAGAACTTTGTCGCGATGG 626
Db 4960 ---AGACCGCGCGGTCGCGAGCGCGAGCTGCGCGATGAGGCGTTCTGCGCACTGA 4905
Qy 627 AGCAGTTTCGCGACCGGACTCTCATGATGATCATAGCGAAGACCGGTTTGTTC 686
Db 4904 GCGGCTCTTCGACTCGCGCAGATCACCGACCGGCTGTGCGCGCGCGGATTCGTGCC 4845
Qy 687 CAATGTGGTTTCGAATCATGAACTCAACCGCTGCGAGGCTGTGTCAGCGAGGTT 746
Db 4844 GCGGCTCTTCGAGAGACCGAGCTGAGCAGCTGCGGCGCTTGGTCCCGCGGCT 4785
Qy 747 CGCGGTTGGTGGTTC 764
Db 4784 CGGTGTGGCGTCCGCC 4767

RESULT 2

US-09-940-316B-1/c

; Sequence 1, Application US/09940316B

; Patent No. 6759536

; GENERAL INFORMATION:

; APPLICANT: KOSAN BIOSCIENCES, Inc.

; APPLICANT: REEVES, CHRISTOPHER

; APPLICANT: CHU, DANIEL

; APPLICANT: KHOSLA, CHAITAN

; APPLICANT: SANTI, DANIEL

; APPLICANT: WU, KAI

; TITLE OF INVENTION: POLYKETIDES ENCODING THE fkbA GENE OF THE PK-520 POLYKETIDE SYNTH

; FILE REFERENCE: 30062-20026.11

; CURRENT APPLICATION NUMBER: US/09/940,316B

; CURRENT FILING DATE: 2001-08-27

; PRIOR APPLICATION NUMBER: 09/410,551

; PRIOR FILING DATE: 1999-10-01

; PRIOR APPLICATION NUMBER: US 60/139,650

; PRIOR FILING DATE: 1999-06-17

; PRIOR APPLICATION NUMBER: US 60/123,810

; PRIOR FILING DATE: 1999-03-11

; PRIOR APPLICATION NUMBER: US 60/102,748

; PRIOR FILING DATE: 1998-10-02

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 77536

; TYPE: DNA

; ORGANISM: Streptomyces hygroscopicus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (52275) ... (71465)

US-09-940-316B-1

Query Match 13.9%; Score 129.6; DB 4; Length 77536;

Best Local Similarity 50.7%; Pred. No. 4.3e-28;

Matches 374; Conservative 0; Mismatches 349; Indels 15; Gaps 2;

Qy 27 CTTGGCACTTGATGGTCCCGAACTTATCCGAATTCGCGCGCAACCCCAAGT 86
Db 5489 CATGAGATACGGGAGTTCGAGTGTTCACGGCTTGGCCGAGCAGCAGTACCAT 5430
Qy 87 AACTGCCGAAGATTAGGCATCCCGAGCCACACTTTTCAGAGCAATCAGCCGAGTGA 146
Db 5429 CACCGCGAAACGGCTCAACATCTCCAGCCGACCTGTCCAGGGGCATCCGCGGCTGA 5370
Qy 147 AAAACACGCGACCCCACTTTTCGACCGCGCGCGCGCGCAAACTGCTCTCAACCAAG 206
Db 5369 GCGAGAGTGGCGTGGCGCTGTTCGACCGGCAACGAAACCGGCTCCGGCTCAACAAGTA 5310
Qy 207 AGGCCACGCTTCTCAACACGCGCGCATCGTCGAGAAATTCAACTCCGCGCAAC 266
Db 5309 CGCGAGTCTTCGCGCGCAGCGCGCTCGCGCGCATGAGTCTCCGCGCGCAGCA 5250
Qy 267 TGAATCAACCGCTCATGAGCCCGAGCAAAAGGCAAAATCCGACTGGACTTCAATGATTC 326
Db 5249 GCGCATACCGCCCTGATGACCGCGCAGCACCGGACCGTGGCACTGGGTTTCTGCACTC 5190
Qy 327 CTTGGCACTTGATGGTCCCGAACTTATCCGAATTCGCGCGCGCGCAACCCCAAGT 386
Db 5189 CTAGGCACTGGTGGTGGCGGCTGTGCTGTCTCCACCGGACACCGGCTGGCTCCCGGCAC 5130
Qy 387 AGAATTCGAATCCCAAGCGCGCAGCAATGCTCTGTGTAGATCGTGTTCGCTGATGA 446
Db 5129 CACCTTCGAATCGCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5070
Qy 447 AACTGACCTCGCATAGTTAGTTGGCCCAACCTCGCGAGGTGTGATCTTTAGGGTGGC 506
Db 5069 GCTGACCTCGGGCTGACAGCCCAACGACCGCGGCTGTGCGCGCGCGGATTCGTGCC 5016
Qy 507 GCACCTGCTTCGTCACGACTTGCCTAGCTGTCCCGCAGATCACCGGCTTGCCTT 566
Db 5015 ACACCTGCGGACGAGGCACTGTGCTGTCTGCTCCACCGGACACCGGCTGGCC----- 4961
Qy 567 TTCTGCGCAAGAGAAATTCGCGTGAATTAATCTCGCGGAGAACTTTGTCGCGATGG 626
Db 4960 ---AGACCGCGCGGTCGCGAGCGCGAGCTGCGCGATGAGGCGTTCTGCGCACTGA 4905
Qy 627 AGCAGTTTCGCGACCGGACTCTCATGATGATCATAGCGAAGACCGGTTTGTTC 686
Db 4904 GCGGCTCTTCGACTCGCGCAGATCACCGACCGGCTGTGCGCGCGCGGATTCGTGCC 4845
Qy 687 CAATGTGGTTTCGAATCATGAACTCAACCGCTGCGAGGCTGTGTCAGCGAGGTT 746
Db 4844 GCGGCTCTTCGAGAGACCGAGCTGAGCAGCTGCGGCGCTTGGTCCCGCGGCT 4785
Qy 747 CGCGGTTGGTGGTTC 764
Db 4784 CGGTGTGGCGTCCGCC 4767

RESULT 3

US-09-252-991A-12324

; Sequence 12324, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

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; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12324
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12324

Query Match          7.3%; Score 68; DB 4; Length 927;
Best Local Similarity 49.2%; Pred. No. 2.4e-10;
Matches 179; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

Qy  38  ACGACCTACGAGCTTCATTTTCAGTCCTCAATCAGGCGCACCTCACCAGAACTGCCGAAA 97
Db  44  ACAGCCTCAACACCGCTTCATCGCCATTCCGAGAGCCGGCAGCTTCTCCGAAGCGCGGAGC 103
Qy  98  GATTAGGCATCCCGCAGCCCCACACTTTCCAGAGCAATCAGCGGAGTGGAATAACACGCAG 157
Db  104  GCCTGCACCTGACCCCAACCGGGGTGAGCAGCGCATCGCGGCCCTCGAACAGAGGCTCA 163
Qy  158  GCACCCCACTTTTTCAGCCGGCGCGCGCAAACTCGTCCTCAACCAACGAGGCGCACGCCCT 217
Db  164  ATGCCCGGCTGTTTCGACCGGGTCGGCGCGAGGTCACCTCACCGAGGCCGCGCGGCC 223
Qy  218  TCCTCAACACGCGCAGCGCCATCGTCGCGAATTCAACTCCGCGCGCACTGAAATCAAAC 277
Db  224  TGCTGCCGCGCGCTACAGTTGCTCAACGTGCTCGACGACACCCGCGGGCGCTGAACA 283
Qy  278  GCCTCATGGACCCAGAAAGGACACATCCGACTGGACTTCATGCATTCTTGGGCACATT 337
Db  284  ACCTCACGGCGAGGTGAGCGGGCGGTGTCCTGGCGCACCGACCAATCGGCTGCG 343
Qy  338  GGATGTGTCGCCGAACATTATCCGAACATTTCCGCGCGCGAAACACCCCAACGTAAGATTCCAAC 397
Db  344  ATCGCTGTCGCGCGCTGCTCTGGCGGCTTTCACCCGGGCGCATTCGCGAGGTGGCGCTGGATA 403
Qy  398  TCCA 401
Db  404  TCCA 407

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RESULT 4
US-09-252-991A-12096/c
; Sequence 12096, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12096
; LENGTH: 972
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12096

```

	Query Match	7.3%	Score 68	DB 4	Length 972
	Best Local Similarity	49.2%	Pred. No. 2.4e-10		
	Matches 179	Conservative 0	Mismatches 185	Indels 0	Gaps 0
Qy	38	ACGACCTACCGAGCTTCATTTCAGTCTCAATCAGGCCACCTCACGGAACATGCCGAAA	97		
Db	890	ACAGCCTCAACACCTTCATGCCATTGCCGAGACGGCAGTTCTTCGAAAGCGCGGAGC	831		
Qy	98	GATTAGGCATCCCGCAGCCCAACATTTCCAGACGAATCAGCCGAGTGGAAAAACACGCAG	157		

Db	830	GCCTGCACCTGACGCCAACCGCGGGTGAGCAAGCGCATCGCGCCCTTCGAACACGACGCTCA	771
Qy	158	GCACCCCACTTTTCGACCGCGCCGCGCAAACTCGTCTCTCAACCAACGAGGCCACGCGCT	217
Db	770	ATGCCCGGCTGTTCGACCGGTTCGCGCGGAGGTCAACTCACCGAGGCGCGCGCGCC	711
Qy	218	TCCTCAACACGCGCAGCGCCATCGTCGCAGAAATTCAACTCCGCGCAACTGGAATCAAC	277
Db	710	TGCTGCGCGGCGCTACAGTTGCTCAACGTGTCGACGACACCCGCGGCGCTGAACA	651
Qy	278	GCCTCATGGACCCAGAAAAGGCACAAATCCGACTGGAATTTCATGCAATTCCTTTGGGCATTT	337
Db	650	ACCTCACCGCGAGGTACAGCGCGGTGGTCTTGCCACACAGCCACCACATCGGCCTGC	591
Qy	338	GGATGTGTCCTCCGAATTCATCGAACATTCGCGGCGGACACCCCAACGTAGAAATTCCAAC	397
Db	590	ATCGCTGCGCGCGCTGCTGCGCGCTTACACCGGCGCATCCCGAGGTGGCGCTGGATA	531
Qy	398	TCCA 401	
Db	530	TCCA 527	

RESULT 5
 US-09-252-991A-12421
 ; Sequence 12421, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 12421
 ; LENGTH: 1482
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-12421

	Query Match	7.3%; Score 68; DB 4; Length 1482;	
	Best Local Similarity	49.2%; Pred. No. 3e-10;	
	Matches 179; Conservative 0; Mismatches 185; Indels 0; Gaps 0		
Qy	38	ACGACCTACGCAGCTTCATTTCACTCGCTCAATCAGGCCACTCACCCGAAACTGCGGAAA	97
Dd	99	ACAGCCTCAAACCTTTCATGCCAATTGCCGAGA CCGGCAGCTTCTCCGAAGCCGGCGGAGC	158
Qy	98	GATTAGGCATCCCCAGCCACACTTTCCACAGCAATCAGCGCGAGTGAAAAACAACGCGAG	157
Dd	159	GCCTGCACCTGACCACACCGCGGTGAGCAAGCATCGCGCCCTCGAACGACGACTCA	218
Qy	158	GCACCCCACTTTTCGACCGCGCCGCGCAAACTCGTCTCTCAA CCACAGAGGCCACGGCT	217
Dd	219	ATGCCCGGCTGTTTCGACCGGCTCGCGCGAGGTCAACTCACCGAGGCGCGCGCGGCC	278
Qy	218	TCCTCAACGAGCGCAGCGCCATCGTCGAGAAATTCACACTCCGCGCGCAACTGAAATCAAC	277
Dd	279	TGCTGCCGCGGCGCTTACAGTTGCTCAACGTGCTCGAGCACCCCGCGGGCGCTGAACA	338
Qy	278	GCCTCATGGACCCAGAAAAAGGCCACAATCCGACTGGACTTCATGCAATTCCTTGGGCACTT	337
Dd	339	ACCTCACCGCGAGGTACAGCGCGGCTGGTCTCTGGCCACCAGGCCACCACTCGSCCTGC	398
Qy	338	GGATGGTCCGGAACCTTATCCGAACATTCGCGCGCGGGAACACCCCAACGTAGNAATCCCAAC	397
Dd	399	ATCGCCTGCGCGCGCTGTCGGCGCCTTACCCGCGGCGCATTCGCGAGTGGCGCTGGATA	458

QY 398 TCCA 401
|||
Db 459 TCCA 462

RESULT 6

US-09-252-991A-7082
; Sequence 7082, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 7082

; LENGTH: 987

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-7082

Query Match 6.6%; Score 61.4; DB 4; Length 987;

Best Local Similarity 47.7%; Pred. No. 2.5e-08;

Matches 179; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

QY 27 CTGCGAATCGACGACCTACGAGCTTCATTTTCAGTCCGCTCAATCAGCGCACTCACC GA 86

Db 78 CTGCGTTTCGACGATATCGAAGCTTCTCAAGTCGCGCACTCAACAGCGTGACGTC 137

QY 87 AACTCCGGAAGATTAGGCATCCCGAGCCCACTTTTCAGACGAATCAGCGAGTGGGA 146

Db 138 GCGCGCCGAGCATGAGCTCTCAAGTCGGTGATCAGCAAGCGTGTGAGGATCTCGA 197

QY 147 AAAACAGCAGCAGCCCACTTTTCAGCGCGCGCGCAACTCGTCTCAACCAAG 206

Db 198 ACGAGCCCTCGCGCTCGCGCTCTATCGCAACCGCAAGCTCGAGCGCAGCGAGGC 257

QY 207 AGGCCAGCGCTTCCTCAACAGCGCAGCGCACTCGTCCGAGAACTCAACTCCGCGCAAC 266

Db 258 CGGGCATTTCTTACNAGCGCGCAAGGCTCTCGTGCAGGAATCAACAGCGCGCGGA 317

QY 267 TGAATCAAAACGCTCATGGACCCAGAAAGGCAATCCGACTGGACTTTCATGCAATTC 326

Db 318 GATTTCGCGCTCGCGAGAACGACTGTGCGGCGAATTTGGCATCGTCAACCCGATGAG 377

QY 327 CTTGGCACTTGGATGGTCCCGAAGTATTCGAACTATCCGAACTCCGCGCGCAACCCCAAGT 386

Db 378 CTTGGCACTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 437

QY 387 AGAATTCCAACTCCA 401

Db 438 GGAGATCGTCTGCA 452

RESULT 7

US-09-252-991A-7058

; Sequence 7058, Application US/09252991A

; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 7058

; LENGTH: 1485

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-7058

Query Match

Best Local Similarity 6.6%; Score 61.4; DB 4; Length 1485;

Matches 179; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

QY 27 CCTCGAATCGACGACCTACGAGCTTCATTTTCAGTCCGCTCAATCAGCGCACTCACC GA 86

Db 124 CTGCGTTTCGACGATATCGAAGCTTCTCTCAAGTCGCGCACTCAACAGCGTGACGTC 183

QY 87 AACTGCCGAAAGATTAGGCATCCCGAGCCCACTTTTCAGACGAATCAGCGAGTGGGA 146

Db 184 GCGCGCCGAGCATGAGCTGTCCAAGTCGGTGATCAGCAAGCGTGTGAGGATCTCGA 243

QY 147 AAAACAGCAGCAGCCCACTTTTCAGCGCGCGCGCAACTCGTCTCAACCAAG 206

Db 244 ACGAGCCCTCGCGCTCGCGCTCTATCGCAACCGCAAGCTCGAGCGCAGCGAGGC 303

QY 207 AGGCCAGCGCTTCCTCAACAGCGCAGCGCACTCGTCCGCAATCAGTCCGCGCAAC 266

Db 304 CGGGCATTTCTTACAGGCGCGCAAGGCTCTCGTGCAGGAATCAACAGCGCGCGGA 363

QY 267 TGAATCAAAACGCTCATGGACCCAGAAAGGCAATCCGACTGGACTTTCATGCAATTC 326

Db 364 GATTTCGCGCTCGCGAGAACGACTGTGCGGCGAATTTGGCATCGTCAACCCGATGAG 423

QY 327 CTTGGCACTTGGATGGTCCCGAAGTATTCGAACTATCCGAACTCCGCGCGCAACCCCAAGT 386

Db 424 CTTGGCACTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483

QY 387 AGAATTCCAACTCCA 401

Db 484 GGAGATCGTCTGCA 498

RESULT 8

US-09-252-991A-7044/c

; Sequence 7044, Application US/09252991A

; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 7044

; LENGTH: 1518

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-7044

Query Match

Best Local Similarity 6.6%; Score 61.4; DB 4; Length 1518;

Matches 179; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

QY 27 CCTCGAATCGACGACCTACGAGCTTCATTTTCAGTCCGCTCAATCAGCGCACTCACC GA 86

Db 1429 CTGCGTTTCGACGATATCGAAGCTTCTCTCAAGTCGCGCACTCAACAGCGTGACGTC 1370

QY 87 AACTGCCGAAAGATTAGGCATCCCGAGCCCACTTTTCAGACGAATCAGCGAGTGGGA 146

Db 1369 GCGCGCCGAGCGCATGAGCCTGTCCAAAGTCGCTGATCAGCAAGCGTGTGAGGATCTCGA 1310
Qy 147 AAAACACGAGCAGCCACTTTTCGACCGCGCGCGCAAACTCGTCTCAACCAAG 206
Db 1309 AGACGCTCGGGTCCGCTGCTCTATCGACCGCGCAAGCTGAGCGCAGCGC 1250
Qy 207 AGGCCACGCTTCTCAACACGCGCAGCGCCATCGTCGAGAAATTCAACTCCGCGCAAC 266
Db 1249 CGGGCACTTTCTCAAGAGCGCGCAAGCGCTCGCTGCAGGAATCTCAACACGCGCGA 1190
Qy 267 TGAATCAACGCTCATGACCGCAGAAAGGCAATCGACTGACTTATGCAATTC 326
Db 1189 GATTGTGCGCCTGCGCGAGACGACCTGTGCGCGAAATTCGCGATGTCACCCCGATGAG 1130
Qy 327 CTGCGCACTTGGATGCTCCCGAACTTATCGAACATTCGCGCGCAACCCCAAGCT 386
Db 1129 CTGCGCACCTGTGCTGTGCGGATCATGCGGACATTCATGAGCAGCACCGCGCT 1070
Qy 387 AGAATTCCAACTCCA 401
Db 1069 GGAGATCGTCTGCA 1055

RESULT 9

US-09-252-991A-13904
; Sequence 13904, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13904
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13904

Query Match 6.4%; Score 59.2; DB 4; Length 1035;
Best Local Similarity 49.5%; Pred. No. 1.2e-07;
Matches 182; Conservative 0; Mismatches 183; Indels 3; Gaps 1;
Qy 39 CGACCTACGCGCTTCATTTCACTGCTCAATCAGCGCCACCTCACCAGAACTGCCGAAAG 98
Db 144 CAGATTCCGCGAGTTTCGTCGCGTTCGCGAGAGCTGAGCTTCGCGCGCGCTGAGCG 203
Qy 99 ATTAGCATCCGCGACCCACACTTTCCAGAGCAATCAGCGAGTGGAAAAACACGCGAG 158
Db 204 CTGACATAGGCGCCAGCCACCGCTGACCACTCGATCGCGCGCTGGAAGAAGTCCG 263
Qy 159 CACCCCACTTTTCGACCGCGCGCGCGCAAACTGCTCTCAACCAAGAGGCGCAAGCTT 218
Db 264 CGCGAGCTGCTGGAGCGTGACAACTGATCCACCGCTGACCGCGCGCGCGCGCTT 323
Qy 219 CTTCAACACGCGCGCGCATCGTCGAGAAATTCACCTCGCGCGCAACTGAAATCAACG 278
Db 324 CTTGACGAGGCGCGCGCGCACCTTGGCCCGAGCGCAACCGCTGCGCGG---CGCGCG 380
Qy 279 CTTGATGAGCCGAGAAAAAGGCAATTCGACTTGGACTTTCATGCAATTCCTTGGCACTTG 338
Db 381 CAGCGCGCGCGAGCGAGCAAGCTTGGCGCTGGGCTGCTGCGACGACCATCATAT 440
Qy 339 GATGTCCTCGCACTTATTCGAACTTCGCGCGCGCAACCCCAACGTAAGATTCACCT 398
Db 441 TCTGCTACCGCGCATCTCCAGCGCTTCGCGCACGAGCATGCGCGCTGCACTTCCAGCT 500

RESULT 10

US-09-252-991A-3008/c
; Sequence 3008, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3008
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3008

Query Match 6.2%; Score 57.8; DB 4; Length 657;
Best Local Similarity 52.7%; Pred. No. 2.5e-07;
Matches 125; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

Qy 27 CCGCGAAATCGAGCAGCTACGAGCTTCAATTTTCAGTCGCTCAATCAGGCGCACCTCACCGA 86
Db 595 CTTGCGCTTGAAGACATACAGGCTTCTCAACGTGTCGAGCTGGGAGCATCAGCGC 536
Qy 87 AACTGCCGAAAGATTAGGCATCCCGAGCCCACTTTCCAGACGAATCAGCGAGTGA 146
Db 535 CGCCGCGGAAACGATGAGCTGTCCAAAGTCCGTGATCAGCAACGCGTCAGCGACCTGA 476
Qy 147 AAAACACGAGCGCACCCCACTTTTCGACCGCGCGCGCAAACTGCTCTCAACCAAG 206
Db 475 GCGCCACCTCGCGCGCTCTCTACCGCTCGACGCGCAACGTCGAGCGCGAGGC 416
Qy 207 AGGCCACGCGCTTCTCAACACGCGCGCGCATCGTCGAGCAATTCACCTCGCGCGC 263
Db 415 CGCGCGCTTCTTCAAGTCGCGCAAGCGCTCGCTGCGAGGACCTGCAACAGCCGC 359

RESULT 11

US-09-252-991A-2667
; Sequence 2667, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2667
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1046)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.

US-09-252-991A-2667

Query Match 6.2%; Score 57.8; DB 4; Length 1074;
Best Local Similarity 52.7%; Pred. No. 3.2e-07;
Matches 125; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 27 CTGCGAATTCGACGACCTACGAGCTTTCATTTTCAGTCGCTCAATCAGGCCACCTCACCGA 86
|||||
Db 165 CTGCGCCTTGAAGACATACAGCCTTCTCAACGTGTGCGAGCTGGCGAGCATCAGCGC 224
|||||

QY 87 AACTGCGGAAGATTAGGATCCCGAGCCCAACATTTCCAGACGAATCAGCCGAGTGA 146
|||||
Db 225 CGCCGCCGAACGATGAGCTGTCCAAGTCGTGATCAGCAACCGTCAGCGACCTGA 284
|||||

QY 147 AAAACACGACGACGCCACCTTTTCGACGCGCGCGCGCAACTCGTCCTCAACCAAG 206
|||||
Db 285 GGGCACCTCGCGGTGCGCTGCTTACCGCTCGACGCGCAACGTGCGAGCGACCGAGGC 344
|||||

QY 207 AGGCCACGCTTCTCAACACCGCCAGCGGCCATCGTCGAGAAATTCAACTCGCGCGC 263
|||||
Db 345 CGCGCGCTTCTCAACAGTCGCGCCAGGCGCTCGTCGAGACCTGAACACGCGCGC 401
|||||

RESULT 12

US-09-252-991A-5341
; Sequence 5341, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5341
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5341

Query Match 6.2%; Score 57.4; DB 4; Length 471;
Best Local Similarity 53.3%; Pred. No. 2.8e-07;
Matches 121; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 35 TCGACGACCTACGAGCTTTCATTTTCAGTCGCTCAATCAGGCCACCTCACCGAACTGCGG 94
|||||
Db 166 TCGACTGCTCGGGTATTTCAGTTCGCGCGCGCGCAACTGCTTACCGTGCCTGCGCGG 225
|||||

QY 95 AAAGATTAGGCATCCCGAGCCCAACATTTTCAGACGAATCAGCCGAGTGGAAAAACAG 154
|||||
Db 226 AGGAACCTGGGACCAACCCAGCTCGGTTCAGCAGCAGATCAACGCTGGAGAAAGAGC 285
|||||

QY 155 CAGGACCCCACTTTTCGACCGCGCGCGCGCAAACTGCTCTCAACCAACGAGCCACG 214
|||||
Db 286 TGGCGACCCCTCTGTTCAGCGCGCTTCATCGAGGCATCGTGTCTACCGACGCGCGCCAGC 345
|||||

QY 215 CTTCTCTCAACCAACGCGCGCATCTCGCAGAAATTCAACTCGCGCC 261
|||||
Db 346 TTCTGCTCGGCACGCTGGCGCGCGCTCGAGACATCGATCGCCGC 392
|||||

RESULT 13

US-09-252-991A-5279
; Sequence 5279, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5279
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5279

Query Match 6.2%; Score 57.4; DB 4; Length 552;
Best Local Similarity 53.3%; Pred. No. 3e-07;
Matches 121; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 35 TCGACGACCTACGAGCTTTCATTTTCAGTCGCTCAATCAGGCCACCTCACCGAACTGCGG 94
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Db 66 TCGACCTGCTCGGGTATTTCAGTTCGCGCGCGCGCAACTCAGTTTACCCTGCGCGG 125
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QY 95 AAAGATTAGGCATCCCGAGCCCAACATTTTCAGACGAATCAGCCGAGTGGAAAAACAG 154
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Db 126 AGGAACCTGGGACCAACCCAGCTCGGTTCAGCAGCAGATCAACGCTGGAGAAAGAGC 185
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QY 155 CAGGACCCCACTTTTCGACCGCGCGCGCGCAAACTGCTCTCAACCAACGAGCCACG 214
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Db 186 TGGCGACCCCTCTGTTCAGCGCGCTTCATCGAGGCATCGTGTCTACCGACGCGCGCCAGC 245
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QY 215 CTTCTCTCAACCAACGCGCGCATCTCGCAGAAATTCAACTCGCGCC 261
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Db 246 TTCTGCTCGGCACGCTGGCGCGCGCTCGAGACATCGATCGCCGC 292
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RESULT 14

US-09-252-991A-5304
; Sequence 5304, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5304
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5304

Query Match 6.2%; Score 57.4; DB 4; Length 909;
Best Local Similarity 53.3%; Pred. No. 3.9e-07;
Matches 121; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 35 TCGACGACCTACGAGCTTTCATTTTCAGTCGCTCAATCAGGCCACCTCACCGAACTGCGG 94
|||||
Db 23 TCGACCTGCTCGGGTATTTCAGTTCGCGCGCGCGCAACTCAGTTTACCCTGCGCGG 82
|||||

QY 95 AAAGATTAGGCATCCCGAGCCCAACATTTTCAGACGAATCAGCCGAGTGGAAAAACAG 154
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Db 83 AGGAACCTGGGACCAACCCAGCTCGGTTCAGCAGCAGATCAACGCTGGAGAAAGAGC 142
|||||

QY 155 CAGGACCCCACTTTTCGACCGCGCGCGCGCAAACTGCTCTCAACCAACGAGCCACG 214
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Db 143 TGGCGACCCCTCTGTTCAGCGCGCTTCATCGAGGCATCGTGTCTACCGACGCGCGCCAGC 202
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Job time : 209 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Perfect score: 930

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Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

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Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
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- 19: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
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- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	930	100.0	3309400	9	US-09-738-626-1
3	924	99.4	924	9	US-09-738-626-3228
4	439	47.2	439	9	US-09-826-909-3
5	129.6	13.9	77536	10	US-09-940-316B-1
6	110.4	11.9	951	15	US-10-156-761-3347
7	110.4	11.9	9025608	15	US-10-156-761-1
8	99.8	10.7	9025608	15	US-10-156-761-1
9	97.8	10.5	936	15	US-10-156-761-1506
10	74.6	8.0	936	15	US-10-156-761-4774
11	71.4	7.7	891	15	US-10-156-761-7285

12	62.6	6.7	894	15	US-10-156-761-4980	Sequence 4980, Ap
13	60.4	6.5	1008	15	US-10-156-761-3218	Sequence 3218, Ap
14	60.2	6.5	876	15	US-10-156-761-1152	Sequence 1152, Ap
15	60	6.5	891	17	US-10-282-122A-31440	Sequence 31440, A
16	59.8	6.4	954	17	US-10-282-122A-14715	Sequence 14715, A
17	59.6	6.4	987	15	US-10-156-761-2141	Sequence 2141, Ap
18	57.8	6.2	882	9	US-09-738-626-473	Sequence 473, App
19	57.6	6.2	1675	9	US-09-938-641-1	Sequence 1, Appli
20	57.6	6.2	3309400	9	US-09-738-626-1	Sequence 1, Appli
21	57.2	6.2	31248	19	US-10-485-710-1	Sequence 1, Appli
22	57.2	6.2	35359	19	US-10-485-710-2	Sequence 2, Appli
23	56.6	6.1	981	9	US-09-738-626-2114	Sequence 2114, Ap
24	56	6.0	888	17	US-10-398-221-2042	Sequence 2042, Ap
25	56	6.0	319630	17	US-10-398-221-7	Sequence 7, Appli
26	56	6.0	3011208	17	US-10-398-221-2058	Sequence 2058, Ap
27	54.4	5.8	912	15	US-10-156-761-761	Sequence 761, Ap
28	54.4	5.8	1109	17	US-10-398-221-1521	Sequence 1521, Ap
29	54.4	5.8	3259	17	US-10-398-221-3552	Sequence 3552, Ap
30	53.4	5.7	1027	17	US-10-282-122A-24068	Sequence 24068, A
31	52.4	5.6	986	17	US-10-282-122A-13903	Sequence 13903, A
32	52	5.6	897	9	US-09-815-242-4087	Sequence 4087, Ap
33	52	5.6	897	17	US-10-282-122A-7352	Sequence 7352, Ap
34	51.8	5.6	3390	9	US-09-767-878-1	Sequence 1, Appli
35	51.2	5.5	1830121	17	US-10-329-670-1	Sequence 1, Appli
36	51.2	5.5	1830121	18	US-10-158-865-1	Sequence 1, Appli
37	50.2	5.4	80161	17	US-10-329-148A-1	Sequence 15044, A
38	49.6	5.3	867	17	US-10-282-122A-15044	Sequence 249, App
39	49.4	5.3	762	9	US-09-738-626-249	Sequence 29, Appl
40	49.4	5.3	892	19	US-10-495-066-29	Sequence 1, Appli
41	49	5.3	2731748	18	US-10-297-465A-1	Sequence 1491, Ap
42	48.8	5.2	312	9	US-09-974-300-1491	Sequence 1, Appli
43	48.2	5.2	30000	11	US-09-980-217-1	Sequence 676, App
44	46.8	5.0	909	9	US-09-738-626-676	Sequence 53, Appl
45	46.8	5.0	1039	18	US-10-494-672-53	

ALIGNMENTS

RESULT 1
US-09-826-909-1
; Sequence 1, Application US/09826909
; Patent No. US20020081674A1
; GENERAL INFORMATION:
; APPLICANT: MOECKEL, BETTINA
; APPLICANT: FARWICK, MIKE
; APPLICANT: HERMANN, THOMAS
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: PFEFFERLE, WALTER
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES FOR ENCODING OF THE LYSR2-GENE
; FILE REFERENCE: 205551US0X
; CURRENT APPLICATION NUMBER: US/09/826,909
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: DE 100 39 047.1
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: DE 100 10 346.8
; PRIOR FILING DATE: 2001-03-03
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1364
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1161)
; OTHER INFORMATION:
US-09-826-909-1
Query Match 100.0%; Score 930; DB 9; Length 1364;
Best Local Similarity 100.0%; Pred. No. 9.9e-293;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 232 GTGACCATGGGCAACGACGGCGGAGACCTGCGAATCGACGACCTACGAGCTTCAATTTCA 291
QY 61 GTGCTCTAATCAGGCGACCTCAACGAAATCGCGAAGATTAGGCAATCCCGAGGCCACA 120
Db 292 GTGCTCTAATCAGGCGACCTCAACGAAATCGCGAAGATTAGGCAATCCCGAGGCCACA 351
QY 121 CTTTCCAGAGATCAGCGAGTGGAAAAACAGGCGAGGACCCCACTTTTCAGCGGCC 180
Db 352 CTTTCCAGAGATCAGCGAGTGGAAAAACAGGCGAGGACCCCACTTTTCAGCGGCC 411
QY 181 GCGCGCAAACTCGTCTCTCAACCAACGAGGCCACGCTTCTCAACCAAGCGCGCCATC 240
Db 412 GCGCGCAAACTCGTCTCTCAACCAACGAGGCCACGCTTCTCAACCAAGCGCGCCATC 471
QY 241 GTGCGAGAATTCAATTCGCGCCCAACTGAAATCAAAAGCTTCATGAGCCAGAAAAAGGC 300
Db 472 GTGCGAGAATTCAATTCGCGCCCAACTGAAATCAAAAGCTTCATGAGCCAGAAAAAGGC 531
QY 301 ACAATCCGACTGACTTCAATGATGATCTTCTTGGGCACTTGGATGTCGCCGAACTTATCGA 360
Db 532 ACAATCCGACTGACTTCAATGATGATCTTCTTGGGCACTTGGATGTCGCCGAACTTATCGA 591
QY 361 ACAATCCGCGCGCAACACACCCCAAGTAGAATTCCTCACTCCACCAAGCGCGCAATGCTC 420
Db 592 ACAATCCGCGCGCAACACACCCCAAGTAGAATTCCTCACTCCACCAAGCGCGCAATGCTC 651
QY 421 CTGGTAGATCGTGTGTTGGCTGATGAATCGACTGCACTGCAATGATTGGCCCCCAAACTGCC 480
Db 652 CTGGTAGATCGTGTGTTGGCTGATGAATCGACTGCACTGCAATGATTGGCCCCCAAACTGCC 711
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QY 541 CCGCGAGATCACCGGCTTCCCTTCTGCGCAAGGAGAAATGCGCTTGATTACTGCG 600
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QY 601 GGGGAAGAACCTTTGTGCGGATGAGAGAGGTTTCGGCAACCGCACTCTCTCATGATGCA 660
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Db 892 TTAGCCGAGAGACCGGTTTCTGTCATGTTGTTTCCGATGTTTCCGATGATGATCGTAC 951
QY 721 GTGCGAGGCTTGTGAGCGAGGCTCTCGCGGTTGTTGTTGTTTCCGATGATGATCGTAC 780
Db 952 GTGCGAGGCTTGTGAGCGAGGCTCTCGCGGTTGTTGTTGTTTCCGATGATGATCGTAC 1011
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Db 1012 CTTTCCACAGTGGGAATCGTGCAACGCGCCACTTAGTCCACCGCTTTATAGGGAATAGGT 1071
QY 841 TTGGTGTGCGCACTCAACGCGGGCGGCACTGCGGTGGATACTTCGGAGTTCGTG 900
Db 1072 TTGGTGTGCGCACTCAACGCGGGCGGCACTGCGGTGGATACTTCGGAGTTCGTG 1131
QY 901 GCGGGATCGAGGTATGCAATTAGAAAGGCGC 930
Db 1132 GCGGGATCGAGGTATGCAATTAGAAAGGCGC 1161
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RESULT 2

US-09-738-626-1/c

; Sequence 1, Application US/09738626

; Publication No. US20020197605A1

; GENERAL INFORMATION:

; APPLICANT: NAKAGAWA, SATOSHI

; APPLICANT: MIZOGUCHI, HIROSHI

; APPLICANT: ANDO, SEIKO

```
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1
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Query Match 100.0%; Score 930; DB 9; Length 3309400;
Best Local Similarity 100.0%; Pred. No. 1.7e-291;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCATGGGCAACGACGGCGGAGACCTGCGAATCGACGACCTACGAGCTTCAATTTCA 60
Db 3128423 GTGACCATGGGCAACGACGGCGGAGACCTGCGAATCGACGACCTACGAGCTTCAATTTCA 3128364
QY 61 GTGCTCTAATCAGGCGACCTCAACGAAATCGCGAAGATTAGGCAATCCCGAGGCCACA 120
Db 3128363 GTGCTCTAATCAGGCGACCTCAACGAAATCGCGAAGATTAGGCAATCCCGAGGCCACA 3128304
QY 121 CTTTCCAGAGATCAGCGAGTGGAAAAACAGGCGAGGACCCCACTTTTCAGCGGCC 180
Db 3128303 CTTTCCAGAGATCAGCGAGTGGAAAAACAGGCGAGGACCCCACTTTTCAGCGGCC 3128244
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Db 3128183 GTGCGAGAATTCAATCGCGCGCAACTGAAATCAAAAGCTTCATGAGCCAGCAAGAAAGGC 3128124
QY 301 ACAATCCGACTGAGCTTCAATGCTTGGGCACTTGGATGTTCCCGAATTTATCCGA 360
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QY 361 ACAATCCGCGCGCAACACCCCAAGTAGAATTCCAACTCCACCAAGCGCGCAATGCTC 420
Db 3128063 ACAATCCGCGCGCAACACCCCAAGTAGAATTCCAACTCCACCAAGCGCGCAATGCTC 3128004
QY 421 CTGCTAGATCGTGTGTTGGCTGATGAACCTGCACTCGCATTTAGTGGCCCCCAACCTGTC 480
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QY 721 GTCCGACGGCTTGTACAGCGCAGCTCTCGGCGTTGGTGTGGTTCGGATGGATCATCGGTAC 780
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QY 781 CTTCCACAGTGGGAATCGTCAAGCCGCCCACTTAGTCCACCCGCTTTATAGGGAACCTAGGT 840
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QY 901 GCGGGATCGAGGTATGTCATTAGAAGAGGCG 930
DB 3127523 GCGGGATCGAGGTATGTCATTAGAAGAGGCG 3127494

RESULT 3

US-09-738-626-3228

; Sequence 3228, Application US/09738626

; Publication No. US20020197605A1

; GENERAL INFORMATION:

; APPLICANT: NAKAGAWA, SATOSHI

; APPLICANT: MIZOGUCHI, HIROSHI

; APPLICANT: ANDO, SEIKO

; APPLICANT: HAYASHI, MIKIRO

; APPLICANT: OCHIAI, KEIKO

; APPLICANT: YOKOI, HARUHIKO

; APPLICANT: TATEISHI, NAKOHO

; APPLICANT: SENOH, AKIHIRO

; APPLICANT: IKEDA, MASATO

; APPLICANT: OZAKI, AKIO

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-125

; CURRENT APPLICATION NUMBER: US/09/738,626

; CURRENT FILING DATE: 2000-12-18

; PRIOR APPLICATION NUMBER: JP 99/377484

; PRIOR FILING DATE: 1998-12-16

; PRIOR APPLICATION NUMBER: JP 00/159162

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: JP 00/280988

; PRIOR FILING DATE: 2000-08-03

; NUMBER OF SEQ ID NOS: 7059

; SOFTWARE: PatentIn ver. 3.0

; SEQ ID NO 3228

; LENGTH: 924

; TYPE: DNA

; ORGANISM: Corynebacterium glutamicum

US-09-738-626-3228

Query Match

Best Local Similarity 99.4%; Score 924; DB 9; Length 924;

Matches 924; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ATGGGCAACGACGGGGAGACCTGCGAATCGACGACCTACGCGCTTCAATTCAGTCGCT 66
DB 1 ATGGGCAACGACGGGGAGACCTGCGAATCGACGACCTACGCGCTTCAATTCAGTCGCT 60
QY 67 CAATCAGGCGCACCTCAAGAACTGCGAAAGATTAGGCATCCGCGCCCACTTTCC 126
DB 61 CAATCAGGCGCACCTCAAGAACTGCGAAAGATTAGGCATCCGCGCCCACTTTCC 120
QY 127 AGACGAATCAGCGAGTGGAAACACGCGAGCACCCCACTTTTCGACCGCGCGCGCGC 186
DB 121 AGACGAATCAGCGAGTGGAAACACGCGAGCACCCCACTTTTCGACCGCGCGCGCGC 180
QY 187 AAATCGTCCTCAACCAAGGCGCACGCTTCTCAACGCGCGCGCGCATCGTCGA 246
DB 181 AAATCGTCCTCAACCAAGGCGCACGCTTCTCAACGCGCGCGCGCATCGTCGA 240

RESULT 4

US-09-826-909-3

; Sequence 3, Application US/09826909

; Patent No. US20020081674A1

; GENERAL INFORMATION:

; APPLICANT: MOECKEL, BETTINA

; APPLICANT: FARWICK, MIKE

; APPLICANT: HERMANN, THOMAS

; APPLICANT: KREUTZER, CAROLINE

; APPLICANT: PFEFFERLE, WALTER

; TITLE OF INVENTION: NUCLEOTIDE

; FILE REFERENCE: 205551US0X

; CURRENT APPLICATION NUMBER: US/09/826,909

; CURRENT FILING DATE: 2002-05-01

; PRIOR APPLICATION NUMBER: DE 100 39 047.1

; PRIOR FILING DATE: 2000-08-10

; PRIOR APPLICATION NUMBER: DE 100 100 346.8

; PRIOR FILING DATE: 2001-03-03

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 439

; TYPE: DNA

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DB 241 GAAATTCATCCGCGCAACTGAAATCAAAACGCTCATGGACCCAGAAAAAGGCAATC 300
QY 307 CGACTGGACTTCATCATCTCTTGGGCACTTGGATGGTCCCGAACTTATCCGAACATTC 366
DB 301 CGACTGGACTTCATCATCTCTTGGGCACTTGGATGGTCCCGAACTTATCCGAACATTC 360
QY 367 CGCGCGCAACACCCCAAGTGAATTCACCTCCCAAGCGCGAGCAATGCTCTTGGA 426
DB 361 CGCGCGCAACACCCCAAGTGAATTCACCTCCCAAGCGCGAGCAATGCTCTTGGA 420
QY 427 GATCGTGTGTTGGCTGATGAACCTGACCTCGCATTTAGTTGGCCCCCAAACTCCCGAGTT 486
DB 421 GATCGTGTGTTGGCTGATGAACCTGACCTCGCATTTAGTTGGCCCCCAAACTCCCGAGTT 480
QY 487 GGTACCTCTTTAGGTTGGCGGCACTGCTTGGTCAACGACTTGCCTAGCTGTTCGCGA 546
DB 481 GGTACCTCTTTAGGTTGGCGGCACTGCTTGGTCAACGACTTGCCTAGCTGTTCGCGA 540
QY 547 GATCACCGGCTTGCCTCTCTTTCTGGCCAAAGGAGAAATTGCGCTTGATTTACTCGCGGAA 606
DB 541 GATCACCGGCTTGCCTCTCTTTCTGGCCAAAGGAGAAATTGCGCTTGATTTACTCGCGGAA 600
QY 607 GAACTCTTTCGTGGCGATCGAGCAGGTTTCGGCACTCCGCACTCCTCATGGATGCTTAGCC 666
DB 601 GAACTCTTTCGTGGCGATCGAGCAGGTTTCGGCACTCCGCACTCCTCATGGATGCTTAGCC 660
QY 667 GAAGAAGCGGTTTGTTCCTCAATGTGGTTTCGAATCCATGGAACTCACACCGTCGCA 726
DB 661 GAAGAAGCGGTTTGTTCCTCAATGTGGTTTCGAATCCATGGAACTCACACCGTCGCA 720
QY 727 GGGCTTGTGACGCGCAGGTCGCGGCTTGGTTCGATGCGATGATGATTCGCTTCCC 786
DB 721 GGGCTTGTGACGCGCAGGTCGCGGCTTGGTTCGATGCGATGATGATTCGCTTCCC 780
QY 787 ACAGTGGGAATCGTGCAACGCGCCACTTAGTCCACCGCTTATAGGGAACCTAGGTTTGGTG 846
DB 781 ACAGTGGGAATCGTGCAACGCGCCACTTAGTCCACCGCTTATAGGGAACCTAGGTTTGGTG 840
QY 847 TGGCGACTCAACGCGGCGCGGCACTCGGCTGGATTAATCTCCGGAAGTTCTGCGCGGA 906
DB 841 TGGCGACTCAACGCGGCGCGGCACTCGGCTGGATTAATCTCCGGAAGTTCTGCGCGGA 900
QY 907 TCGAGGTATGATTAGAGAGGCG 930
DB 901 TCGAGGTATGATTAGAGAGGCG 924

RESULT 4

US-09-826-909-3

; Sequence 3, Application US/09826909

; Patent No. US20020081674A1

; GENERAL INFORMATION:

; APPLICANT: MOECKEL, BETTINA

; APPLICANT: FARWICK, MIKE

; APPLICANT: HERMANN, THOMAS

; APPLICANT: KREUTZER, CAROLINE

; APPLICANT: PFEFFERLE, WALTER

; TITLE OF INVENTION: NUCLEOTIDE

; FILE REFERENCE: 205551US0X

; CURRENT APPLICATION NUMBER: US/09/826,909

; CURRENT FILING DATE: 2002-05-01

; PRIOR APPLICATION NUMBER: DE 100 39 047.1

; PRIOR FILING DATE: 2000-08-10

; PRIOR APPLICATION NUMBER: DE 100 100 346.8

; PRIOR FILING DATE: 2001-03-03

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 439

; TYPE: DNA

; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 3347
; LENGTH: 951
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(951)
US-10-156-761-3347

Query Match 11.9%; Score 110.4; DB 15; Length 951;
Best Local Similarity 48.4%; Pred. No. 4.2e-25;
Matches 411; Conservative 0; Mismatches 421; Indels 18; Gaps 3;
QY 51 CTTCAATTTTCAGTCGCTCAATCAGGCCACCTCACCGAAACTGCGGAAAGATTAGGATCC 110
DB 90 CTTCCCGGGTGGCCGACGACGTCACCCGGCGCGGAGGAGTGCAGTCC 149
QY 111 GCAGCCACATTTCCAGAGCAATCAGCGGAGTGGAATAACAGCAGGACCCCACTTTT 170
DB 150 GCAGTCCACCTCTCCCGCTCCCTCGCTCGGCTCGAGCAGGACCTGGGCGTGCACCTTT 209
QY 171 GCAGCGCGCGCGCGCAACTCGTCTCAACCAACAGGCGCACGCTTCTCAACACGCG 230
DB 210 CGCCCGCGCGCGCGACGCTCTCGCTCACCCGGCGCGGCTACGTTCTCTCGCTCGT 269
QY 231 CAGCGCCCATCTGCGCAGAAATTCAACTCCCGCAACTGAAATCAAAACGCTCATGGAACC 290
DB 270 CGAGCGCGCTCGCGAGATCGAGCGGCGCGCGAGGTCGCGCGGACCGCACCC 329
QY 291 AGAAAAAGCAAAATCCGATCGGACTTCATGCAATTCCTTGGGCACTTGGATGGTCCCGA 350
DB 330 GGCACCGCGAAGTTCGCTTCGGCTTCTGACACCACTGGGCTCGAGACCGTGCCTGG 389
QY 351 ACTTATCCGAATTCGCGCGCGACACCCCAACCTAGAAATCCAACTCCACCAAGCGCG 410
DB 390 GCTGATCCGAGCTTCGCGCGCGATCATCCGCGCTCGGCTTCAGCGCTCGTCAGAACTA 449
QY 411 AGCAATGCTCTGCTAGATCGTGTGTTTGGCTGATGAACTGACCTCGCATTAGTTGGGCC 470
DB 450 CGCGAGGCGATGATCGAGCGGCTCGGCGCGGGGAGTTGGACCTCTGTCTGACCTCGC 509
QY 471 CAAACCTGCGAGGTTGTACTCTTTTAGGGTGGGCGGCACCTGCTTCTGCAACGACTTGC 530
DB 510 CGTGCAGGACGCGC-----CGACCTGGTGGCGCGGCTCGACGAGCAAGCTGGG 563
QY 531 CTAAGCTTTCGCGAGATCAACGCTTGCCTCTTTCTGCGCAAGGAAATTCGCTT 590
DB 564 GCTCTGCTGCTCGCGCGCACACCGCTCGCCGCAACGCAAGCGC-----GTGGGCT 614
QY 591 GATTACTGCGCGGAAGAACCTTTCGTGCGATGCGAGCAGGTTTCGGCACCCGACTCT 650
DB 615 CGCCGAGGCGCGAGACACTTCTGTGACCTCGAACCCGGTTAGGGCTCGCGGAT 674
QY 651 CATGATGATTTAGCGAAGAGCGGTTTGTTCCTCAATGTTGTTTTCGAATCCATGA 710
DB 675 CACCGACGAGCTGCGCAGGAGCGGTTTTCAGACCGCGCATCGCTTCGAGGCGGAG 734
QY 711 ACTCACCGCTGCGAGGCTTTCAGCGCAGGCTTCGCGGTTGGTGGTTCCGATGA 770
DB 735 GCGGAGAGCTACGCGGCTTGTGCGCGCGGCTCGGGGTCGCGCTCTCTCGCGCAC 794
QY 771 TCATCGTACCTTCCACAGTGGAACTCGTGAAACGCCCACTTAGTCCACCGCTTATAG 830
DB 795 GCGCGTCCCGCGGAGTTG----TCGAGCTGAGGCTACGCGCCCGCGCGGTCG 851
QY 831 GGAACCTAGGTTTGGTGGAGCTCAACCGCGGCGCGCACCTGCGGTGGATAACTTCG 890

DB 852 CGAGATCGGCTCGCTCGCTGCGACCGCCACACCGCGGTGGCGGCTTCAA 911
QY 891 GAAATTCGTG 900
DB 912 GAAATTCGTG 921
RESULT 7
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
Query Match 11.9%; Score 110.4; DB 15; Length 9025608;
Best Local Similarity 48.4%; Pred. No. 1.2e-23;
Matches 411; Conservative 0; Mismatches 421; Indels 18; Gaps 3;
QY 51 CTTCAATTTTCAGTCGCTCAATCAGGCCACCTCACCGAAACTGCGGAAAGATTAGGATCC 110
DB 4176160 CTTCCCGGGTGGCGCGACGTCACCGCGCGCGGAGGATGCAGTCC 4176101
QY 111 GCAGCCACACTTTCAGACGAAATCAGCGGAGTGAAAAACAGCAGGACCCCACTTTT 170
DB 4176100 GCAGTCCACCTCTCCCGCTCCCTCGCTCGAGGAGCTGGGGCTCGACCTTT 4176041
QY 171 CGACCGCGCGCGCAAACTCGTCTCAACCAACGAGGCCACGCTTCTCAACACCGC 230
DB 4176040 CGCCCGCGCGCGCGACGCTCGCTCACCCCGCGCGCGTATGTTCTCGCTCGCT 4175981
QY 231 CAGCGCCATCTGTCGAGAAATCACTCCGCGCAACTGAAATCAAAACGCTCATGACCC 290
DB 4175980 CGAGCGCGCTCGCGGAGATCGAGCGGCGCGCGAGGTCGCGCGCGGACCC 4175921
QY 291 AGAAAAAGCAATTCGACTGGACTTCATGCAATTCCTTGGGCACTTGGATGGTCCCGA 350
DB 4175920 GCGCACCGGCAAGTTCGCTTTCGCTTTCGACACCACTGGGCTCGAGACCTGCGCGG 4175861
QY 351 ACTTATCCGAACATTCGCGCGCAACCCCAACCTAGAAATTCCAACTCCACCAAGCGCG 410
DB 4175860 GCTGATCCGAGCTTCCGCGCGCATCTCCGCGCTCGCTTTCAGCTCGTCAGAACTA 4175801
QY 411 AGCAATGCTCTGCTAGATCGTGTGTTTGGCTGATGAACTGACCTCGCATTAGTTGGCCC 470
DB 4175800 CGCGGAGGAGTATCGAGCGGCTCGGCGCGGGAGTTGGACCTCTGTCTGACCTCGCG 4175741
QY 471 CAAACCTGCGAGGTTGGTACTCTTTTAGGGTGGGCGCACCTGCTTCGTCAAGCACTTGC 530

Db	4175740	CGTGCCGGACGCGC-----CCGACCTGGTGGCCCGCGGCTCGACGAGCAGAACTGGC	4175687
Qy	531	CCTAGCTGTTTCCCGCAGATCACCGGCTTGCTCTCTTTCTTGGCCAAGAGAAATTGGCGTT	590
Db	4175686	GCTCGTGTCCCGSCCGACACCGCTCGCGCAGCAGCGC-----GTGCGCCT	4175636
Qy	591	GATTACTGCGCGGAGAAACTTTCTGTGGGATGCGAGCAGGTTTGGCACCAGACTCCT	650
Db	4175635	CGCGAGGCGCGCAGCAGACCTTCTGTGACCTCGAACCCGGTTACGGGTGCGCGGTAT	4175576
Qy	651	CATGGATGCTATTAGCCGAAGAAGCCGGTTTGTTCCTCAATGTGTTTTCGAATCCATGGA	710
Db	4175575	CACCGACAGCTGTGCCACAGAGGCCGGTTTCAGACCGCGCATCGCTTCAGGGCGAGGA	4175516
Qy	711	ACTCACACCGTCGCAAGGCTTGTACGCGAGGTCCTGGCGTTGTGGTTCCTCGATGGA	770
Db	4175515	GGCGGAGACGCTACGGGCGCTGTGTGCGCGCGGGCTCGGCGTCTCGCCCTCTCGCGCCACC	4175456
Qy	771	TGATCCGTACTTCCACAGTGGGAATCGTGCAAGCCCACTTAGTCCACCCGCTTATAG	830
Db	4175455	GGCGGTGCCCGCCGCGAGTTG---TCGAGCTGACGGTCAACGGTCAACGGCCCGCGCGGTCCG	4175399
Qy	831	GGAACTAGGTTTGGTGTGGCGACTCAACGGGGCGCGGACCTCGCGTGGATAACTTCCG	890
Db	4175398	CGAGATCGGCGTGCCTGGCTGGACGGCCACCCGGACACACCGCCGGTGGCCCTTCAA	4175339
Qy	891	GAAGTTCGTG	900
Db	4175338	GAAGTTCCTG	4175329

RESULT 8

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US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 902508
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or
US-10-156-761-1

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	Query Match	10.7%	Score 99.8	DB 15	Length 9025608
	Best Local Similarity	47.0%	Pred. No. 3.5e-20		
	Matches 364	Conservative 0	Mismatches 382	Indels 15	Gaps 2
QY	5	CCATGGGCAACGACGGCGGAGACCTCGAATCGACGACCTACGACCTTCATTTACGTGCG	64		
Db	1859954	CCATGAGGAGGAAGAAATGCACGATCGACCTCCAGGTACTCCGCTCCTTCCAGGCGGTGG	1860013		
QY	65	CTCAATCAGCGCCACTTCACCGAAACTCGCGAAGATTAGGCATCCGCGACGCCACACTTTT	124		
Db	1860014	CAGAGGGAACGACGGTGACCGACGCGCGGCGGACGCCCGTATCACCCACGCGGCCCTGT	1860073		

Qy	125	CCAGACGAATCAGCGAGTGAGAAAAACACGACGAGCACCCCACTTTTCGACCGCGCGCGGCC	184
Db	1860074	CGGGGGCCCTGAAACCCGGCTCGAGGACGAGGTGCGCGCGGAACCTCTTCACAGCGGTGCGGAC	1860133
Qy	185	GCAAACTCGTCCTCAACACGAGGGCAGCGCTTCCTCAACACGCGCAGCGCCATCGTCG	244
Db	1860134	CGGTACTGCGCCTCAACCCGGCCGAGCGGGTGTTCAAGAGATGCTGACGCGGTGCTCG	1860193
Qy	245	CAGAATTCAACTCCGCGCGCACTGAATCAACCGCTCATGGACCCAGAAAAAGGCACAA	304
Db	1860194	ACAGCTACGACCGGGGC CGCGAGCGCGTGCAGAGATCGTCGACCCGGACGCGGGTGCGG	1860253
Qy	305	TCCGACTGGACTTCATGCAATCTCTGGGCACCTGGATGGTCCCGCAACTTATCCGAAACAT	364
Db	1860254	TGTGCTGGCGCTTCTCTGCACACCCCTGGGCACTGGCTGTGGCCAGGCTTGTACGGACT	1860313
Qy	365	TCGCGCGCGAAACCCCACTAGAAATCCAACTCCACCAAGCGGACGAAATGCTCCTGG	424
Db	1860314	TCGGCAGGGGTTCCTCGCAGGCCCGGTTTGAGCTGCACCAGACGCGGAGATCGGACTGA	1860373
Qy	425	TAGATCGTGTTTTGGCTGTAGTAACTGACCTCGCATTAGTTGGCCCCAAACCTGCCGAGG	484
Db	1860374	CCGGGCACCTCTCTGACGCGCACCGCGGACCTGATCATCACCAGCAGCGAGCCCGCCA--	1860431
Qy	485	TTGGTACTCTTTAGGGTGGCGCCACTGCTCGTCAACGACTTGCCTAGCTGTTCCTCG	544
Db	1860432	-----CCCCCTGATCACTGGCGGGCTCTCTGGTGGAGCACTACGGCTGGCGGTCCCCG	1860487
Qy	545	CAGATCACCGGGCTTGCTCCTTTTCTGGCCAAAGGAAATTGCGGTGTGATTACTGCGGCGG	604
Db	1860488	CCGGCACCGCTGGCC-----AGCGGGCGCGGGCCCGTCTGGCCGAGGTGSCCG	1860538
Qy	605	AAGAACCTTTCTGGCGGATCGCAGCAGGTTCCTGGCACCCGACTCCTCATGTGATGCAATTAG	664
Db	1860539	AGGAGCGGTTCATCTCTGCTCAAGCCCGGTTACGGGCTGCGCGGCATCAGCGAGACGTTGT	1860598
Qy	665	CCGAAGAAGCCGGTTTTGTTTCCCAATGTGTTTTCGAATCCATGGAATCACCAACGCTCG	724
Db	1860599	GCCTCGAGGCCGCTTCAACCCCGCTCGTCGGCTTCAGGGCGAGGAGGTGGACCTTGC	1860658
Qy	725	CAGGGCTTGTACGCGCAGGTCTCGGGCTTGGTGTGTTCCG	765
Db	1860659	GGGGCTGTGTGCGCGCGGCTCTGGGTGTGTCCTGATCCCG	1860699

RESULT 9

```

US/10-156-761-1506
; Sequence 1506, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1506
; LENGTH: 936
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS

```

; LOCATION: (1)..(936)
US-10-156-761-1506

Query Match 10.5%; Score 97.8; DB 15; Length 936;
Best Local Similarity 47.7%; Pred. No. 5.5e-21;
Matches 362; Conservative 0; Mismatches 382; Indels 15; Gaps 2;

QY 7 ATGGCAACGACGGCGGAGACTCGGAATCGACGACCTACGAGCTTCATTTCAGTCGCT 66
Db 1 ATGAGGAGGAGAGATGACGATGACCTCCAGGTACTCCGCTCTCCAGGCCGTGGCA 60

QY 67 CAATCAGGACCTCACCAGAACTCGGAAAGATTAGGATCCCGAGCCACATTTCC 126
Db 61 GAGGAAACGACGGTACCGACCGCCGCGGAGCGCCGTATCACCCAGCCGCGCTGTG 120

QY 127 AGACGAATCAGCGAGTGGAAAAACAACGAGGACCCCACTTTTCGACCGCGCGCGCG 186
Db 121 CGGCGCTTGAACCGCTCGAGGACGAGTGGCGGCGGAACTTTCCAGGCGTGGAGCG 180

QY 187 AAATCTGCTCTCAACCAAGAGGCGACGCTTCTCAACCAAGCGGCGGCAATCTCGCA 246
Db 181 GTACTGCGCTCACCCGCGCGGAGCGGGTTTCAAGGAGTACGTGACGCGGTGCTGAC 240

QY 247 GAAATCACTCCGCGCACTGAAATCAAAACGCTCATGGACCCAGAAAAGGCAATC 306
Db 241 AGCTAGACCGGCGCGGCGGAGCGCTGGCGAGATCGTCGACCCGCGGCGCGGTG 300

QY 307 CGACTGGACTTCATGATCTCTTGGGCACTTGGATGCTCCCGAACTTATCCGAACATTC 366
Db 301 TGCTGGCGCTTCTGACACCTTGGGCACTTGGTGGTGGCGGAGTGTGACGAGCTTC 360

QY 367 CGCGCGCAACACCCAAAGTAAATTTCCAACTCCACCAAGCGGCGGCAATGCTCTGTA 426
Db 361 CGGCGAGCGGTTCGCGAGCGCGGTTGAGCTGACAGGAGCGGCGGAGTGGACTGACC 420

QY 427 GATCGTGTGTTGGTGTGAATCACTGACTCGCAATTAGTTGGCGCCAAACCTGCGAGTT 486
Db 421 CGGCACTCTCTGAGCGCACCGCGGACCTGATCATCACGAGCGAGCGCGCCCA 476

QY 487 GGTACTCTTTAGGTGGCGCACTGCTTCTGCAAGCACTTGCCTAGCTGCTCCCGCA 546
Db 477 ---CCCTGTATCACCTGGCGGCTCTCTGTTGGAGGCACTACGGGTGGCGCTCCCGCC 534

QY 547 GATCACCGGCTTGCCTCTTTCTGGCCAAAGAGAAATTGCCGTGTGATTACTCGCGCGAA 606
Db 535 CGGCAACCGCTGCGC-----AGGCGCGCGGCGCGCTGCGCGAGTGGCGGAG 585

QY 607 GAACCTTTGTTGGGATGAGAGAGTTTCGGACCGGACTCCTCATGATGATGATAGCC 666
Db 586 GAGCGCTTCATCTGCTCAAGCCCGGTTACGGGCTGCGCGGATCAGCGAGACGTTGTGC 645

QY 667 GAAGAAGCGGTTTCTTCCCAATGTTGTTTTCGAATCCATGAACTCACACCGTCCGA 726
Db 646 CTCGAGGCGGCTTACCCCGCTGCTGCGCTTCGAGGCGGAGGAGTGGAGACCTTGCGG 705

QY 727 GGGCTGTGTCAGCGAGGCTCTCGCGGTTGGTGGTTCCG 765
Db 706 GGCCTGTGTCGCGCGGCTCTGGTGTGCTCCCTGATCCCG 744

RESULT 10
US-10-156-761-4774
; Sequence 4774, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4774
; LENGTH: 936
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(936)
US-10-156-761-4774

Query Match 8.0%; Score 74.6; DB 15; Length 936;
Best Local Similarity 44.7%; Pred. No. 2.1e-13;
Matches 342; Conservative 0; Mismatches 414; Indels 9; Gaps 1;

QY 5 CCATGGGCAACGACGGCGGAGACCTGCGAAATCGACGACTACGCAAGCTTCATTTCAGTCG 64
Db 17 CCATGAATCAGAACGATGCGCGCTGGATCTCCAGCAGATGCGATACGTCTGTCGCGCTG 76

QY 65 CTCATATCAGGCGACCTCAACGAAACTGCCGAAAGATTAGGCATCCGCGAGCCACACTTT 124
Db 77 CGGAAACCGCAACTTCAACCGCGCGCGGAGCGTGTCTCGTGGTGCAGTCTGCTCACTCA 136

QY 125 CAGACGAAATCAGCGAGTGGAAAAACAGCAGGACCCCACTTTTCAGCCGCGGCGCC 184
Db 137 GTCACCGATCGCGGCTCGGAAACGCGAGCTCGGGGTCAAGCTGTTCGCCCGATCCAGC 196

QY 185 GCAAACTCTCTCAACCAACGAGGCGCACGCTTCTCAACCAACGAGCGCATCTGTCG 244
Db 197 GCGGCTCGAGTACAGCGCGGAGCGGCTTCTCTGTCGCGCGCGGAGTGGCTGG 256

QY 245 CAGAAATCAACTCGCGCAACTGAAATCAAAAGCTCATGGACCCGAGAAAAGGCAAA 304
Db 257 CGCTGCGACCGCGCGCTTGCAGATCTGCGGCGCGACCGCGCTGTGTACGCGGCGGCG 316

QY 305 TCCGACTGCACTTATGCACTTCTTGGGCACTTGGATGGTCCCCCACTTATCCGAACT 364
Db 317 TCGCGTCTGGGCTGATCGTGACCGCTGCGCTGACGTACCCGAGTTGTCGACGCGT 376

QY 365 TCGCGCGCAACACCCCAAGTAGAATTCRAACTCCACCAAGCGCGAGCAATGCTCTCGG 424
Db 377 ACCGCGCCAGCACCCGAGACGTCATGCTCTGCTCCGTTCCGGGCGCAGCAGCACTGG 436

QY 425 TAGATCGTGTGTTGCTGATGAACTGACCTCGCAATTAGTTGGCCCCCAAACTGCGGAGG 484
Db 437 TGGCGCGATCCGGAACCGGAACTGGACATCGCCTTCTCTGGTTGCGGAGGCGAAC 496

QY 485 TTGCTACCTCTTTAGGTTGGCGCCACCTGCTTCGTCAGCACTTGCCTAGCTGTTCCTCG 544
Db 497 GCGCACCCGCTGTGAAACCGTTGTTCTCGATCACGACGACACGCTACTGTTGGTGGCGG 556

QY 545 CAGATCACCGCTTCCCTCTTTCTGGCAAGGAGAAATTGCGCTTGTATTACTGCGCGCG 604
Db 557 CCGGGCACCGGCTCGGGGTGTCTC-----CCAGGTACGCTGCGGAGATGCGCG 607

QY 605 AAGAACTTTTCTGGCGGATGCGAGCAGGTTTCGGCACCCGACTCTCTCATGATGATAG 664
Db 608 AGGAGACGTACGTGGACTTCGTGGCGGAGACCCCGCGGCGCCAGTCCGATCAGCGCT 667

QY 665 CCGAAGAGCGGTTTGTTCCTCAATGTGTTTTCGAATCCATGGAATTCACACCGCTCG 724
Db 668 TCGCGCTCGCGGCTGTGTCGCGACGTCGCGTACGAGGCGGCTGTCTGCTGAGCTGATCA 727

QY 725 CAGGCTTGTACGCGCAGGCTCTCGGCTTGGTGTGTTCCGATGG 769
Db 728 CCGGTTGATCACGCGCGGCTCGCATGCGCTGCTGCTCGCTGG 772

Query Match	6.7%;	Score 62.6;	DB 15;	Length 894;
Best Local Similarity	43.9%;	Pred. No. 1.7e-09;		
Matches 318;	Conservative 0;	Mismatches 404;	Indels 3;	Gaps 1;
Qy	41	ACCTAGCAGCTTCATTTTCAGTCGCTCAATCAGGCCACCTCACCGAAACTGCCGAAAGAT	100	
Db	17	ATCTCGCGGTGTGGTTCGCGTGCGCCACCGGCTCTTTCTCGCGCGGGGGCGCGAGC	76	
Qy	101	TAGGCATCCCGCAGCCACACATTTTCAGAGCAATCAGCCGAGTGGAAAAACACCCAGGCA	160	
Db	77	TGGGCTGCACCCAGCCGCGCTCAGCCAGCAGATGAAGGCGCTGGAGTCGTCGTTGGCA	136	
Qy	161	CCCCATTTTCGACCGCGCGCGCGCAAACTGTCCTCAACCAAGGAGCCACGCCCTTC	220	
Db	137	CACCGCTGCTGATCCGACCGGGCGGAAATGGCCCTGACCCAGCGCGGCGAGGCCCTTG	196	
Qy	221	TCAACCAAGCCAGGCGCATCGTCGAGAAATCAACTCCGCGCAACTGAAATCAAAAGCC	280	
Db	197	TCCGGCACGCCCGGGGATCATCGCGGATCTACGGCGCGCGAGGAGAGGTCCGCGCA	256	
Qy	281	TCATGACCCAGAAAAAGGCACAATCCGACTGGACTTCATGCAFTCTTGGGCACATTGGA	340	
Db	257	TCGCGGACTTCGCGCGGCGCGGTAGTCTCGTCTGTTCCACGGCAGTTCCGGCG	316	
Qy	341	TGTTCCCGCAACTTATCCGAACAATTCGCGCGCGCAACACCCCAACGTAGAAATCCAACTCC	400	
Db	317	TCGTCCCGACCGCCCTGGCCGCTCTGGCGCGCGCACCCCGGCACCCGGGTCTCCCTGG	376	

QY 401 ACCAAGGGGAGCAATGCTCTCTGGTAGATCGTGTGTTTGGTGATGAATGACCTCGCAT 460
Db 377 AGAGGCGCAACCGCGCGCTCGGTGAGATGCTGCGGAGGCGGACTGCGATGTGGCGC 436
QY 461 TAGTTGGCCCAACCTGCGGAGGTTGGTACCTCTTTAGGGTGGGCGCCACTGCTTCGNC 520
Db 437 TCGCTTCCGGTACGAGGTTGCGCGCGCGCGAGAAATGGAGCACTTGGTGTACGCC 496
QY 521 AAGCACTTCCCTAGCTGTTCCGCGAGATCACCGGCTTGCTCTCTTTCTTGGCCAGGAG 580
Db 497 CCTGTCTACCGACCTGCTCGTCCGCTGCTGCTCCCGAGGGCACCGGCTGCGCGACCG 556
QY 581 AATTGCGGTGATTACTCGGCGGAAGAACTTTCTGTCGCGATCGAGCAGGTTTCGGA 640
Db 557 A--GTCCGTCGCCATCGCGGACCTCGCGCGGACCGGTGGATCGCGGATGCCCGCT 613
QY 641 CCGGACTCTCTATGATGATCATAGCCGAAGAGCGGTTTGTTCCTCAATGTGTTTCG 700
Db 614 GCGCGGTGAGTCTGCTGAGGTGTGCGAGAGCGCGGCTTCACTCCCGGATCGACTTCG 673
QY 701 AATCCATGGAATCACACCGTGCAGGGCTTGTTCAGCGCAGGCTCTCGCGTGTGGTGG 760
Db 674 CGACCGAGCACTACCGCGGCTGCTGCTGCTGAGCGCGGCTCTCGCGTGGCGGTAC 733
QY 761 TTCCG 765
Db 734 TGCCG 738

RESULT 13

US-10-156-761-3218

; Sequence 3218, Application US/10156761

; Publication No. US20030119018A1

; GENERAL INFORMATION:

; APPLICANT: OMURA, SATOSHI

; APPLICANT: IKEDA, HARUO

; APPLICANT: ISHIKAWA, JUN

; APPLICANT: HORIKAWA, HIROSHI

; APPLICANT: SHIBA, TADAYOSHI

; APPLICANT: SAKAKI, YOSHIYUKI

; APPLICANT: HATTORI, MASAHIRA

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-262

; CURRENT APPLICATION NUMBER: US/10/156,761

; PRIOR FILING DATE: 2002-05-29

; PRIOR APPLICATION NUMBER: JP 2001-204089

; PRIOR FILING DATE: 2001-05-30

; PRIOR APPLICATION NUMBER: JP 2001-272697

; PRIOR FILING DATE: 2001-08-02

; NUMBER OF SEQ ID NOS: 15109

; SEQ ID NO 3218

; LENGTH: 1008

; TYPE: DNA

; ORGANISM: Streptomyces avermitilis

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1008)

US-10-156-761-3218

Query Match

Best Local Similarity 6.5%; Score 60.4; DB 15; Length 1008;

Matches 190; Conservative 0; Mismatches 216; Indels 0; Gaps 0;

QY 1 GTGACATGGGCAACGACGGCGGAGACCTCGCAATCGACGACCTACGAGCTTCATTCA 60
Db 7 GGGACACGAGCAACGGGCGGCGCCAGCCAGCTTCGCCAGCTCGGGGCTTCGCGGCC 66
QY 61 GTGCTCAATCAGGGCCACTCACCGAAATGCGGAAAGATTAGGATCCCGCAGGCCACA 120
Db 67 GTGCGGAGCATCTGACTTCGCGACGCGGCGCGCGATCGGATGAGCAGCGCGG 126
QY 121 CTTTTCAGAGCAATCAGCGAGTGGAAACACGAGGCAACCCCACTTTTCAGCGGCC 180

Db 127 CTGTGCGGCGCGGTCTCGCCCTTGAGAGAGACACTCGGGGTGACCTCTCTCGAGCGTACG 186
QY 181 GGCCGCAAACTCGTCTCAACCAACGAGGCGCACGCTTCTCTCAACCAACGAGCGCATC 240
Db 187 ACCCGNAGGTCTGCTCTCGCCCGCGGTGCGCGTCTCGCGTAGCGCCAGGCGGTG 246
QY 241 GTGCGAGAAATCAACTCGCCCGCAACTGAAATCAACGCTCATGGACCCAGAAAAAGGC 300
Db 247 CTGCGAGAGGTGCGGCGCGCTGATGAGGAGGCGGAGGCGGTACGCGCCCGTTTCA 306
QY 301 ACAATCCGACTGACTTCAATGCTTGGGCACTTGGATGGTCCCGCAACTTATCCGA 360
Db 307 GCGCTGCGGCTCGGGGTGATCCCACTCGCGCGTATCTGCTGCGGACCGTCTCAGG 366
QY 361 ACATTCGCGCGCAACACCCCAACGTAGAAATTCCAACTCCACCAAG 406
Db 367 CTCGTCCAGACCGGTACCCCGACCTCGACCTCCAGGTCCACGAGG 412

RESULT 14

US-10-156-761-1152

; Sequence 1152, Application US/10156761

; Publication No. US20030119018A1

; GENERAL INFORMATION:

; APPLICANT: OMURA, SATOSHI

; APPLICANT: IKEDA, HARUO

; APPLICANT: ISHIKAWA, JUN

; APPLICANT: HORIKAWA, HIROSHI

; APPLICANT: SHIBA, TADAYOSHI

; APPLICANT: SAKAKI, YOSHIYUKI

; APPLICANT: HATTORI, MASAHIRA

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-262

; CURRENT APPLICATION NUMBER: US/10/156,761

; CURRENT FILING DATE: 2002-05-29

; PRIOR APPLICATION NUMBER: JP 2001-204089

; PRIOR FILING DATE: 2001-05-30

; PRIOR APPLICATION NUMBER: JP 2001-272697

; PRIOR FILING DATE: 2001-08-02

; NUMBER OF SEQ ID NOS: 15109

; SEQ ID NO 1152

; LENGTH: 876

; TYPE: DNA

; ORGANISM: Streptomyces avermitilis

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(876)

US-10-156-761-1152

Query Match

Best Local Similarity 6.5%; Score 60.2; DB 15; Length 876;

Matches 203; Conservative 0; Mismatches 238; Indels 0; Gaps 0;

QY 29 TCGGAATCGAGCACTACGAGCTTCATTTTCAGTCGCTCAATTCAGGCGACCTCAGCGAAA 88
Db 2 TGGAACTGCGCACCTTCAGCATTTTCGTCGCGCTCGCGAGGACCGAGCACTTCACCGGG 61
QY 89 CTGCGGAAGATTAGGCATCCGCGAGCCACACTTTCCAGAGCAATCAGCCGAGTGGAAA 148
Db 62 CAGCGAAACGGCTGATGTTGTCGCACTCGGGGCTGTCGCGCTCGATCCGCGCCCTGGAGC 121
QY 149 AACCGCAGGCAACCCCACTTTTCGACCGCGCGCGCAAACTCGTCTCAACCAACGAG 208
Db 122 GGGAGCTCCAGGCGCGCTGTTGTCGCGCACCCCGCAGTGTACGCTCACCGAGGCCG 181
QY 209 GCCAGCCTTCTCAACCAACGCGAGCGCAATGTCGCGAGAAATTCGAATCCGCGCAATG 268
Db 182 GCGCGCGCTGTCGGGCGAGCGAGCGATCTTGGCCAGGTCCGGGCGGCTCAGAGC 241
QY 269 AAATCAACGCTCATGAGCCAGCAAAAGGCAACAAATCGGACTGCACTTCATGCTTCT 328
Db 242 CGGTGGCGCGCGTGCAGGCGGTGCTGTCGCGGCGACGCTCTCGCTGGGCGACCGAGCATGCA 301

QY 329 TGGGCACTTGGATGTCCTCCGAACTTATCCGAACATTCGCGCCGGAACACCCCAACGTAG 388
Db |||||
302 TCGCGGGGTGATGTGGCCCGGCTGCTGCGCGGTTCGCGGGGAGATCCGGATGTGG 361
QY 389 AATTCAACTCCACCAAGCGGAGCAATGCTCTCTGGTAGATCGTGTGTTGGCTGATGAAA 448
Db |||||
362 AGATCCGGTTCGCCAGGCGGGCTCGGGTGGCTGCGGAGGAAGTCGCGCGCGGGCGTC 421
QY 449 CTGACCTCGCATTTAGTTGGCC 469
Db 422 TCGATCTGGCCCTTCGCGGTCC 442

RESULT 15

US-10-282-122A-31440
; Sequence 31440, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Lianguo
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31440
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Pseudomonas putida
US-10-282-122A-31440

Query Match 6.5%; Score 60; DB 17; Length 891;
Best Local Similarity 46.4%; Pred. No. 1.2e-08;
Matches 195; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY 38 ACGACCTACGAGCTTCACTTTTCAGTCGCTCAATCAGGCCACCTCACCGAACTGCCGAAA 97
Db |||||
17 AAGACATCAGATCTTTCGTGAAATCGCGAATCGGGCAGTTTCATGAGCGCCCGGAAG 76
QY 98 GATTAGGCATCCCGAGCCCACTTTCCAGACGAATCAGCCGAGTGGAAGAAACACGCAG 157
|||

Db 77 CGTCCACTTGTTCGCCAGCCGCCCTGAGCCGACGGATCAAGAAGCTGGAGGAAGSCCTGG 136
QY 158 GCACCCCACTTTTGGACCGCGCCGGCCGCAAACTCGTCTCTCAACCAACGAGGCCACGCCT 217
Db |||||
137 GCACCTCGCTACTGGAACGCACTCGCCGGGTGAGCTGACCAAGCGTGGGCGCGACT 196
QY 218 TCCTCAACACGCGCAGCGCCATCGTCGAGAAATTCAACTCCGCGCGCAACTGAAATCAAAC 277
Db |||||
197 TCCTGCCCAAGGCCAGGGCCTGCTGGATGATTTTGAAGACTCGATCCTCAGCATCCGG 256
QY 278 GCCTCATGGACCCAGAAAAAGSCAAATCCGACTGGACTTCATGCAATTCCTTTGGSCACTT 337
Db |||||
257 AGCTGGCGAGCGCCAGACCGGTTCAGGTTACCTTCGCTGCAATTCCTACCGCGGCTTCT 316
QY 338 GGATGGTCCCGAACTTATCCGAACATTCGCGCGGGAACACCCCAACGTAGAAATCCAAAC 397
Db |||||
317 ACTTCCTGCGCTCGGTGATCCGCGATTACAAAGAGCAATACCCGAAATTCGCGCATTCGCC 376
QY 398 TCCACCAAGCGGAGCAATGCTCCTGGTAGATCGTGTGCTGATGAAACTGACCTCG 457
Db |||||
377 TGCTGGACCTTAGCGCCAAACGACGCGGCTCGAAGCGGTGCTGCGCGGCGAGGCCGACTTCG 436

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Job time : 633 secs